

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Israel, David
Wolfman, Neil M
- (ii) TITLE OF INVENTION: RECOMBINANT BONE MORPHOGENETIC PROTEIN
HETERODIMERS, COMPOSITIONS AND METHODS OF USE
- (iii) NUMBER OF SEQUENCES: 35
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Legal Affairs, Genetics Institute, Inc.
 - (B) STREET: 87 CambridgePark Drive
 - (C) CITY: Cambridge
 - (D) STATE: MA
 - (E) COUNTRY: USA
 - (F) ZIP: 02140-2387
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/864,692
 - (B) FILING DATE: 07-APR-1992
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Kapinos, Ellen J.
 - (B) REGISTRATION NUMBER: 32,245
 - (C) REFERENCE/DOCKET NUMBER: GI-5192A
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 617 876-1170
 - (B) TELEFAX: 617 876-5851

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1607 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: DNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 356..1543
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTCTGACTCTA GAGTGTGTGT CAGCTTTGG CTGGGGACTT CTTGAACTTCAGGGAGAAT	60
AACTTGCGCA CCCCACTTTG CGCCGGTGCC TTTGCCCCAG CGGAGCCTGC TTCGCCATCT	120
CCGAGCCCCA CCGCCCCTCC ACTCCTCGGC CTTGCCCCGAC ACTGAGACGC TGTTCCCAGC	180
GTGAAAAGAG AGACTGCGCG GCCGGCACCC GGGAGAAGGA GGAGGCAAAG AAAAGGAACG	240
GACATTCGGT CCTTGCGCCA GGTCCTTTGA CCAGAGTTTT TCCATGTGGA CGCTCTTTCA	300
ATGGACGTGT CCCC GCGTGC TTCTTAGACG GACTGCGGTC TCCTAAAGGT CGACC ATG Met 1	358
GTG GCC GGG ACC CGC TGT CTT CTA GCG TTG CTG CTT CCC CAG GTC CTC Val Ala Gly Thr Arg Cys Leu Leu Ala Leu Leu Leu Pro Gln Val Leu 5 10 15	406
CTG GGC GGC GCG GCT GGC CTC GTT CCG GAG CTG GGC CGC AGG AAG TTC Leu Gly Gly Ala Ala Gly Leu Val Pro Glu Leu Gly Arg Arg Lys Phe 20 25 30	454
GCG GCG GCG TCG TCG GGC CGC CCC TCA TCC CAG CCC TCT GAC GAG GTC Ala Ala Ala Ser Ser Gly Arg Pro Ser Ser Gln Pro Ser Asp Glu Val 35 40 45	502
CTG AGC GAG TTC GAG TTG CGG CTG CTC AGC ATG TTC GGC CTG AAA CAG Leu Ser Glu Phe Glu Leu Arg Leu Leu Ser Met Phe Gly Leu Lys Gln 50 55 60 65	550
AGA CCC ACC CCC AGC AGG GAC GCC GTG GTG CCC CCC TAC ATG CTA GAC Arg Pro Thr Pro Ser Arg Asp Ala Val Val Pro Pro Tyr Met Leu Asp 70 75 80	598
CTG TAT CGC AGG CAC TCA GGT CAG CCG GGC TCA CCC GCC CCA GAC CAC Leu Tyr Arg Arg His Ser Gly Gln Pro Gly Ser Pro Ala Pro Asp His 85 90 95	646
CGG TTG GAG AGG GCA GCC AGC CGA GCC AAC ACT GTG CGC AGC TTC CAC Arg Leu Glu Arg Ala Ala Ser Arg Ala Asn Thr Val Arg Ser Phe His 100 105 110	694
CAT GAA GAA TCT TTG GAA GAA CTA CCA GAA ACG AGT GGG AAA ACA ACC His Glu Glu Ser Leu Glu Glu Leu Pro Glu Thr Ser Gly Lys Thr Thr 115 120 125	742
CGG AGA TTC TTC TTT AAT TTA AGT TCT ATC CCC ACG GAG GAG TTT ATC Arg Arg Phe Phe Phe Asn Leu Ser Ser Ile Pro Thr Glu Glu Phe Ile 130 135 140 145	790
ACC TCA GCA GAG CTT CAG GTT TTC CGA GAA CAG ATG CAA GAT GCT TTA Thr Ser Ala Glu Leu Gln Val Phe Arg Glu Gln Met Gln Asp Ala Leu 150 155 160	838
GGA AAC AAT AGC AGT TTC CAT CAC CGA ATT AAT ATT TAT GAA ATC ATA Gly Asn Asn Ser Ser Phe His His Arg Ile Asn Ile Tyr Glu Ile Ile 165 170 175	886
AAA CCT GCA ACA GCC AAC TCG AAA TTC CCC GTG ACC AGA CTT TTG GAC Lys Pro Ala Thr Ala Asn Ser Lys Phe Pro Val Thr Arg Leu Leu Asp	934

180					185					190						
ACC Thr	AGG Arg	TTG Leu	GTG Val	AAT Asn	CAG Gln	AAT Asn	GCA Ala	AGC Ser	AGG Arg	TGG Trp	GAA Glu	ACT Thr	TTT Phe	GAT Asp	GTC Val	982
	195					200					205					
ACC Thr	CCC Pro	GCT Ala	GTG Val	ATG Met	CGG Arg	TGG Trp	ACT Thr	GCA Ala	CAG Gln	GGA Gly	CAC His	GCC Ala	AAC Asn	CAT His	GGA Gly	1030
	210				215					220					225	
TTC Phe	GTG Val	GTG Val	GAA Glu	GTG Val	GCC Ala	CAC His	TTG Leu	GAG Glu	GAG Glu	AAA Lys	CAA Gln	GGT Gly	GTC Val	TCC Ser	AAG Lys	1078
				230					235					240		
AGA Arg	CAT His	GTT Val	AGG Arg	ATA Ile	AGC Ser	AGG Arg	TCT Ser	TTG Leu	CAC His	CAA Gln	GAT Asp	GAA Glu	CAC His	AGC Ser	TGG Trp	1126
			245					250					255			
TCA Ser	CAG Gln	ATA Ile	AGG Arg	CCA Pro	TTG Leu	CTA Leu	GTA Val	ACT Thr	TTT Phe	GGC Gly	CAT His	GAT Asp	GGA Gly	AAA Lys	GGG Gly	1174
		260					265					270				
CAT His	CCT Pro	CTC Leu	CAC His	AAA Lys	AGA Arg	GAA Glu	AAA Lys	CGT Arg	CAA Gln	GCC Ala	AAA Lys	CAC His	AAA Lys	CAG Gln	CGG Arg	1222
	275					280					285					
AAA Lys	CGC Arg	CTT Leu	AAG Lys	TCC Ser	AGC Ser	TGT Cys	AAG Lys	AGA Arg	CAC His	CCT Pro	TTG Leu	TAC Tyr	GTG Val	GAC Asp	TTC Phe	1270
	290				295					300					305	
AGT Ser	GAC Asp	GTG Val	GGG Gly	TGG Trp	AAT Asn	GAC Asp	TGG Trp	ATT Ile	GTG Val	GCT Ala	CCC Pro	CCG Pro	GGG Gly	TAT Tyr	CAC His	1318
				310					315					320		
GCC Ala	TTT Phe	TAC Tyr	TGC Cys	CAC His	GGA Gly	GAA Glu	TGC Cys	CCT Pro	TTT Phe	CCT Pro	CTG Leu	GCT Ala	GAT Asp	CAT His	CTG Leu	1366
			325					330					335			
AAC Asn	TCC Ser	ACT Thr	AAT Asn	CAT His	GCC Ala	ATT Ile	GTT Val	CAG Gln	ACG Thr	TTG Leu	GTC Val	AAC Asn	TCT Ser	GTT Val	AAC Asn	1414
		340					345					350				
TCT Ser	AAG Lys	ATT Ile	CCT Pro	AAG Lys	GCA Ala	TGC Cys	TGT Cys	GTC Val	CCG Pro	ACA Thr	GAA Glu	CTC Leu	AGT Ser	GCT Ala	ATC Ile	1462
	355					360					365					
TCG Ser	ATG Met	CTG Leu	TAC Tyr	CTT Leu	GAC Asp	GAG Glu	AAT Asn	GAA Glu	AAG Lys	GTT Val	GTA Val	TTA Leu	AAG Lys	AAC Asn	TAT Tyr	1510
	370				375					380					385	
CAG Gln	GAC Asp	ATG Met	GTT Val	GTG Val	GAG Glu	GGT Gly	TGT Cys	GGG Gly	TGT Cys	CGC Arg	TAGTACAGCA AAATTAAATA				1563	
				390				395								
CATAAATATA TATATATATA TATATTTTAG AAAAAAGAAA AAAA																1607

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Val	Ala	Gly	Thr	Arg	Cys	Leu	Leu	Ala	Leu	Leu	Leu	Pro	Gln	Val	
1				5					10					15		
Leu	Leu	Gly	Gly	Ala	Ala	Gly	Leu	Val	Pro	Glu	Leu	Gly	Arg	Arg	Lys	
			20					25					30			
Phe	Ala	Ala	Ala	Ser	Ser	Gly	Arg	Pro	Ser	Ser	Gln	Pro	Ser	Asp	Glu	
		35					40					45				
Val	Leu	Ser	Glu	Phe	Glu	Leu	Arg	Leu	Leu	Ser	Met	Phe	Gly	Leu	Lys	
	50					55					60					
Gln	Arg	Pro	Thr	Pro	Ser	Arg	Asp	Ala	Val	Val	Pro	Pro	Tyr	Met	Leu	
65					70					75					80	
Asp	Leu	Tyr	Arg	Arg	His	Ser	Gly	Gln	Pro	Gly	Ser	Pro	Ala	Pro	Asp	
				85					90					95		
His	Arg	Leu	Glu	Arg	Ala	Ala	Ser	Arg	Ala	Asn	Thr	Val	Arg	Ser	Phe	
			100					105					110			
His	His	Glu	Glu	Ser	Leu	Glu	Glu	Leu	Pro	Glu	Thr	Ser	Gly	Lys	Thr	
		115					120					125				
Thr	Arg	Arg	Phe	Phe	Phe	Asn	Leu	Ser	Ser	Ile	Pro	Thr	Glu	Glu	Phe	
	130					135					140					
Ile	Thr	Ser	Ala	Glu	Leu	Gln	Val	Phe	Arg	Glu	Gln	Met	Gln	Asp	Ala	
145					150					155					160	
Leu	Gly	Asn	Asn	Ser	Ser	Phe	His	His	Arg	Ile	Asn	Ile	Tyr	Glu	Ile	
				165					170					175		
Ile	Lys	Pro	Ala	Thr	Ala	Asn	Ser	Lys	Phe	Pro	Val	Thr	Arg	Leu	Leu	
			180					185					190			
Asp	Thr	Arg	Leu	Val	Asn	Gln	Asn	Ala	Ser	Arg	Trp	Glu	Thr	Phe	Asp	
		195					200					205				
Val	Thr	Pro	Ala	Val	Met	Arg	Trp	Thr	Ala	Gln	Gly	His	Ala	Asn	His	
	210					215					220					
Gly	Phe	Val	Val	Glu	Val	Ala	His	Leu	Glu	Glu	Lys	Gln	Gly	Val	Ser	
225					230					235					240	
Lys	Arg	His	Val	Arg	Ile	Ser	Arg	Ser	Leu	His	Gln	Asp	Glu	His	Ser	
				245					250					255		
Trp	Ser	Gln	Ile	Arg	Pro	Leu	Leu	Val	Thr	Phe	Gly	His	Asp	Gly	Lys	
			260					265					270			
Gly	His	Pro	Leu	His	Lys	Arg	Glu	Lys	Arg	Gln	Ala	Lys	His	Lys	Gln	

275

280

285

Arg Lys Arg Leu Lys Ser Ser Cys Lys Arg His Pro Leu Tyr Val Asp
 290 295 300
 Phe Ser Asp Val Gly Trp Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr
 305 310 315 320
 His Ala Phe Tyr Cys His Gly Glu Cys Pro Phe Pro Leu Ala Asp His
 325 330 335
 Leu Asn Ser Thr Asn His Ala Ile Val Gln Thr Leu Val Asn Ser Val
 340 345 350
 Asn Ser Lys Ile Pro Lys Ala Cys Cys Val Pro Thr Glu Leu Ser Ala
 355 360 365
 Ile Ser Met Leu Tyr Leu Asp Glu Asn Glu Lys Val Val Leu Lys Asn
 370 375 380
 Tyr Gln Asp Met Val Val Glu Gly Cys Gly Cys Arg
 385 390 395

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1954 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 403..1626

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTCTAGAGGG CAGAGGAGGA GGGAGGGAGG GAAGGAGCGC GGAGCCCGGC CCGGAAGCTA	60
GGTGAGTGTG GCATCCGAGC TGAGGGACGC GAGCCTGAGA CGCCGCTGCT GCTCCGGCTG	120
AGTATCTAGC TTGTCTCCCC GATGGGATTC CCGTCCAAGC TATCTCGAGC CTGCAGCGCC	180
ACAGTCCCCG GCCCTCGCCC AGGTTCACCTG CAACCGTTCA GAGGTCCCCA GGAGCTGCTG	240
CTGGCGAGCC CGCTACTGCA GGGACCTATG GAGCCATTCC GTAGTGCCAT CCCGAGCAAC	300
GCACTGCTGC AGCTTCCCTG AGCCTTTCCA GCAAGTTTGT TCAAGATTGG CTGTCAAGAA	360
TCATGGACTG TTATTATATG CCTTGTTTTC TGTCAAGACA CC ATG ATT CCT GGT	414
Met Ile Pro Gly	
1	
AAC CGA ATG CTG ATG GTC GTT TTA TTA TGC CAA GTC CTG CTA GGA GGC	462
Asn Arg Met Leu Met Val Val Leu Leu Cys Gln Val Leu Leu Gly Gly	
5 10 15 20	

GCG Ala	AGC Ser	CAT His	GCT Ala	AGT Ser 25	TTG Leu	ATA Ile	CCT Pro	GAG Glu	ACG Thr 30	GGG Gly	AAG Lys	AAA Lys	AAA Lys	GTC Val 35	GCC Ala	510
GAG Glu	ATT Ile	CAG Gln 40	GGC Gly	CAC His	GCG Ala	GGA Gly	GGA Gly	CGC Arg 45	CGC Arg	TCA Ser	GGG Gly	CAG Gln 50	AGC Ser	CAT His	GAG Glu	558
CTC Leu	CTG Leu	CGG Arg 55	GAC Asp	TTC Phe	GAG Glu	GCG Ala	ACA Thr 60	CTT Leu	CTG Leu	CAG Gln	ATG Met	TTT Phe 65	GGG Gly	CTG Leu	CGC Arg	606
CGC Arg	CGC Arg 70	CCG Pro	CAG Gln	CCT Pro	AGC Ser	AAG Lys 75	AGT Ser	GCC Ala	GTC Val	ATT Ile	CCG Pro 80	GAC Asp	TAC Tyr	ATG Met	CGG Arg	654
GAT Asp 85	CTT Leu	TAC Tyr	CGG Arg	CTT Leu	CAG Gln 90	TCT Ser	GGG Gly	GAG Glu	GAG Glu	GAG Glu 95	GAA Glu	GAG Glu	CAG Gln	ATC Ile	CAC His 100	702
AGC Ser	ACT Thr	GGT Gly	CTT Leu 105	GAG Glu	TAT Tyr	CCT Pro	GAG Glu	CGC Arg	CCG Pro 110	GCC Ala	AGC Ser	CGG Arg	GCC Ala	AAC Asn 115	ACC Thr	750
GTG Val	AGG Arg	AGC Ser 120	TTC Phe	CAC His	CAC His	GAA Glu	GAA Glu	CAT His 125	CTG Leu	GAG Glu	AAC Asn	ATC Ile	CCA Pro 130	GGG Gly	ACC Thr	798
AGT Ser	GAA Glu 135	AAC Asn	TCT Ser	GCT Ala	TTT Phe	CGT Arg	TTC Phe 140	CTC Leu	TTT Phe	AAC Asn	CTC Leu 145	AGC Ser	AGC Ser	ATC Ile	CCT Pro	846
GAG Glu 150	AAC Asn	GAG Glu	GTG Val	ATC Ile	TCC Ser	TCT Ser 155	GCA Ala	GAG Glu	CTT Leu	CGG Arg 160	CTC Leu	TTC Phe	CGG Arg	GAG Glu	CAG Gln	894
GTG Val 165	GAC Asp	CAG Gln	GGC Gly	CCT Pro	GAT Asp 170	TGG Trp	GAA Glu	AGG Arg	GGC Gly 175	TTC Phe	CAC His	CGT Arg	ATA Ile	AAC Asn	ATT Ile 180	942
TAT Tyr	GAG Glu	GTT Val	ATG Met	AAG Lys 185	CCC Pro	CCA Pro	GCA Ala	GAA Glu	GTG Val 190	GTG Val	CCT Pro	GGG Gly	CAC His	CTC Leu 195	ATC Ile	990
ACA Thr	CGA Arg	CTA Leu 200	CTG Leu	GAC Asp	ACG Thr	AGA Arg	CTG Leu	GTC Val 205	CAC His	CAC His	AAT Asn	GTG Val 210	ACA Thr	CGG Arg	TGG Trp	1038
GAA Glu	ACT Thr 215	TTT Phe	GAT Asp	GTG Val	AGC Ser	CCT Pro	GCG Ala 220	GTC Val	CTT Leu	CGC Arg	TGG Trp 225	ACC Thr	CGG Arg	GAG Glu	AAG Lys	1086
CAG Gln 230	CCA Pro	AAC Asn	TAT Tyr	GGG Gly	CTA Leu	GCC Ala 235	ATT Ile	GAG Glu	GTG Val	ACT Thr 240	CAC His	CTC Leu	CAT His	CAG Gln	ACT Thr	1134
CGG Arg 245	ACC Thr	CAC His	CAG Gln	GGC Gly	CAG Gln 250	CAT His	GTC Val	AGG Arg	ATT Ile 255	AGC Ser	CGA Arg	TCG Ser	TTA Leu	CCT Pro	CAA Gln 260	1182

GGG AGT GGG AAT TGG GCC CAG CTC CGG CCC CTC CTG GTC ACC TTT GGC	1230
Gly Ser Gly Asn Trp Ala Gln Leu Arg Pro Leu Leu Val Thr Phe Gly	
265 270 275	
CAT GAT GGC CGG GGC CAT GCC TTG ACC CGA CGC CGG AGG GCC AAG CGT	1278
His Asp Gly Arg Gly His Ala Leu Thr Arg Arg Arg Arg Ala Lys Arg	
280 285 290	
AGC CCT AAG CAT CAC TCA CAG CGG GCC AGG AAG AAG AAT AAG AAC TGC	1326
Ser Pro Lys His His Ser Gln Arg Ala Arg Lys Lys Asn Lys Asn Cys	
295 300 305	
CGG CGC CAC TCG CTC TAT GTG GAC TTC AGC GAT GTG GGC TGG AAT GAC	1374
Arg Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn Asp	
310 315 320	
TGG ATT GTG GCC CCA CCA GGC TAC CAG GCC TTC TAC TGC CAT GGG GAC	1422
Trp Ile Val Ala Pro Pro Gly Tyr Gln Ala Phe Tyr Cys His Gly Asp	
325 330 335 340	
TGC CCC TTT CCA CTG GCT GAC CAC CTC AAC TCA ACC AAC CAT GCC ATT	1470
Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala Ile	
345 350 355	
GTG CAG ACC CTG GTC AAT TCT GTC AAT TCC AGT ATC CCC AAA GCC TGT	1518
Val Gln Thr Leu Val Asn Ser Val Asn Ser Ser Ile Pro Lys Ala Cys	
360 365 370	
TGT GTG CCC ACT GAA CTG AGT GCC ATC TCC ATG CTG TAC CTG GAT GAG	1566
Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp Glu	
375 380 385	
TAT GAT AAG GTG GTA CTG AAA AAT TAT CAG GAG ATG GTA GTA GAG GGA	1614
Tyr Asp Lys Val Val Leu Lys Asn Tyr Gln Glu Met Val Val Glu Gly	
390 395 400	
TGT GGG TGC CGC TGAGATCAGG CAGTCCTTGA GGATAGACAG ATATACACAC	1666
Cys Gly Cys Arg	
405	
CACACACACA CACCACATAC ACCACACACA CACGTTCCCA TCCACTCACC CACACACTAC	1726
ACAGACTGCT TCCTTATAGC TGGACTTTTA TTTAAAAAAA AAAAAAATAA AATGGAAAAA	1786
ATCCCTAAAC ATTCACCTTG ACCTTATTTA TGACTTTACG TGCAAATGTT TTGACCATAT	1846
TGATCATATA TTTTGACAAA ATATATTTAT AACTACGTAT TAAAAGAAAA AAATAAAATG	1906
AGTCATTATT TTAAAAAATA AAAAAAAACT CTAGAGTCGA CGGAATTC	1954

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Ile	Pro	Gly	Asn	Arg	Met	Leu	Met	Val	Val	Leu	Leu	Cys	Gln	Val	
1				5					10					15		
Leu	Leu	Gly	Gly	Ala	Ser	His	Ala	Ser	Leu	Ile	Pro	Glu	Thr	Gly	Lys	
			20					25					30			
Lys	Lys	Val	Ala	Glu	Ile	Gln	Gly	His	Ala	Gly	Gly	Arg	Arg	Ser	Gly	
		35					40					45				
Gln	Ser	His	Glu	Leu	Leu	Arg	Asp	Phe	Glu	Ala	Thr	Leu	Leu	Gln	Met	
	50					55					60					
Phe	Gly	Leu	Arg	Arg	Arg	Pro	Gln	Pro	Ser	Lys	Ser	Ala	Val	Ile	Pro	
65					70					75					80	
Asp	Tyr	Met	Arg	Asp	Leu	Tyr	Arg	Leu	Gln	Ser	Gly	Glu	Glu	Glu	Glu	
				85					90					95		
Glu	Gln	Ile	His	Ser	Thr	Gly	Leu	Glu	Tyr	Pro	Glu	Arg	Pro	Ala	Ser	
			100					105					110			
Arg	Ala	Asn	Thr	Val	Arg	Ser	Phe	His	His	Glu	Glu	His	Leu	Glu	Asn	
		115					120					125				
Ile	Pro	Gly	Thr	Ser	Glu	Asn	Ser	Ala	Phe	Arg	Phe	Leu	Phe	Asn	Leu	
	130					135					140					
Ser	Ser	Ile	Pro	Glu	Asn	Glu	Val	Ile	Ser	Ser	Ala	Glu	Leu	Arg	Leu	
145					150					155					160	
Phe	Arg	Glu	Gln	Val	Asp	Gln	Gly	Pro	Asp	Trp	Glu	Arg	Gly	Phe	His	
				165					170					175		
Arg	Ile	Asn	Ile	Tyr	Glu	Val	Met	Lys	Pro	Pro	Ala	Glu	Val	Val	Pro	
		180						185					190			
Gly	His	Leu	Ile	Thr	Arg	Leu	Leu	Asp	Thr	Arg	Leu	Val	His	His	Asn	
		195					200					205				
Val	Thr	Arg	Trp	Glu	Thr	Phe	Asp	Val	Ser	Pro	Ala	Val	Leu	Arg	Trp	
	210					215					220					
Thr	Arg	Glu	Lys	Gln	Pro	Asn	Tyr	Gly	Leu	Ala	Ile	Glu	Val	Thr	His	
225					230					235					240	
Leu	His	Gln	Thr	Arg	Thr	His	Gln	Gly	Gln	His	Val	Arg	Ile	Ser	Arg	
				245					250					255		
Ser	Leu	Pro	Gln	Gly	Ser	Gly	Asn	Trp	Ala	Gln	Leu	Arg	Pro	Leu	Leu	
			260					265					270			
Val	Thr	Phe	Gly	His	Asp	Gly	Arg	Gly	His	Ala	Leu	Thr	Arg	Arg	Arg	
		275					280					285				
Arg	Ala	Lys	Arg	Ser	Pro	Lys	His	His	Ser	Gln	Arg	Ala	Arg	Lys	Lys	
	290					295					300					

Asn	Lys	Asn	Cys	Arg	Arg	His	Ser	Leu	Tyr	Val	Asp	Phe	Ser	Asp	Val
305					310					315					320
Gly	Trp	Asn	Asp	Trp	Ile	Val	Ala	Pro	Pro	Gly	Tyr	Gln	Ala	Phe	Tyr
				325					330					335	
Cys	His	Gly	Asp	Cys	Pro	Phe	Pro	Leu	Ala	Asp	His	Leu	Asn	Ser	Thr
			340					345					350		
Asn	His	Ala	Ile	Val	Gln	Thr	Leu	Val	Asn	Ser	Val	Asn	Ser	Ser	Ile
		355					360					365			
Pro	Lys	Ala	Cys	Cys	Val	Pro	Thr	Glu	Leu	Ser	Ala	Ile	Ser	Met	Leu
	370					375					380				
Tyr	Leu	Asp	Glu	Tyr	Asp	Lys	Val	Val	Leu	Lys	Asn	Tyr	Gln	Glu	Met
385					390					395					400
Val	Val	Glu	Gly	Cys	Gly	Cys	Arg								
				405											

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 97..1389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTGACCGAGC	GGCGCGGACG	GCCGCCTGCC	CCCTCTGCCA	CCTGGGGCGG	TGCGGGCCCG		60
GAGCCCGGAG	CCCGGGTAGC	GCGTAGAGCC	GGCGCG	ATG	CAC	GTG	CGC
				Met	His	Val	Arg
				1			5
CGA	GCT	GCG	GCG	CCG	CAC	AGC	TTC
Arg	Ala	Ala	Ala	Pro	His	Ser	Phe
			10				15
CTG	CTG	CGC	TCC	GCC	CTG	GCC	GAC
Leu	Leu	Arg	Ser	Ala	Leu	Ala	Asp
		25				30	
TCG	AGC	TTC	ATC	CAC	CGG	CGC	CTC
Ser	Ser	Phe	Ile	His	Arg	Arg	Leu
		40				45	
CAG	CGC	GAG	ATC	CTC	TCC	ATT	TTG
Gln	Arg	Glu	Ile	Leu	Ser	Ile	Leu
		55				60	
							65
							70

CAC His	CTC Leu	CAG Gln	GGC Gly	AAG Lys 75	CAC His	AAC Asn	TCG Ser	GCA Ala	CCC Pro 80	ATG Met	TTC Phe	ATG Met	CTG Leu	GAC Asp 85	CTG Leu	354
TAC Tyr	AAC Asn	GCC Ala	ATG Met 90	GCG Ala	GTG Val	GAG Glu	GAG Glu	GGC Gly 95	GGC Gly	GGG Gly	CCC Pro	GGC Gly	GGC Gly 100	CAG Gln	GGC Gly	402
TTC Phe	TCC Ser	TAC Tyr 105	CCC Pro	TAC Tyr	AAG Lys	GCC Ala	GTC Val 110	TTC Phe	AGT Ser	ACC Thr	CAG Gln	GGC Gly 115	CCC Pro	CCT Pro	CTG Leu	450
GCC Ala 120	AGC Ser	CTG Leu	CAA Gln	GAT Asp	AGC Ser	CAT His 125	TTC Phe	CTC Leu	ACC Thr	GAC Asp	GCC Ala 130	GAC Asp	ATG Met	GTC Val	ATG Met	498
AGC Ser 135	TTC Phe	GTC Val	AAC Asn	CTC Leu	GTG Val 140	GAA Glu	CAT His	GAC Asp	AAG Lys	GAA Glu 145	TTC Phe	TTC Phe	CAC His	CCA Pro	CGC Arg 150	546
TAC Tyr	CAC His	CAT His	CGA Arg	GAG Glu 155	TTC Phe	CGG Arg	TTT Phe	GAT Asp	CTT Leu 160	TCC Ser	AAG Lys	ATC Ile	CCA Pro	GAA Glu 165	GGG Gly	594
GAA Glu	GCT Ala	GTC Val	ACG Thr 170	GCA Ala	GCC Ala	GAA Glu	TTC Phe	CGG Arg 175	ATC Ile	TAC Tyr	AAG Lys	GAC Asp	TAC Tyr 180	ATC Ile	CGG Arg	642
GAA Glu	CGC Arg	TTC Phe 185	GAC Asp	AAT Asn	GAG Glu	ACG Thr	TTC Phe 190	CGG Arg	ATC Ile	AGC Ser	GTT Val	TAT Tyr 195	CAG Gln	GTG Val	CTC Leu	690
CAG Gln 200	GAG Glu	CAC His	TTG Leu	GGC Gly	AGG Arg	GAA Glu 205	TCG Ser	GAT Asp	CTC Leu	TTC Phe	CTG Leu 210	CTC Leu	GAC Asp	AGC Ser	CGT Arg	738
ACC Thr 215	CTC Leu	TGG Trp	GCC Ala	TCG Ser	GAG Glu 220	GAG Glu	GGC Gly	TGG Trp	CTG Leu	GTG Val 225	TTT Phe	GAC Asp	ATC Ile	ACA Thr	GCC Ala 230	786
ACC Thr	AGC Ser	AAC Asn	CAC His	TGG Trp 235	GTG Val	GTC Val	AAT Asn	CCG Pro	CGG Arg 240	CAC His	AAC Asn	CTG Leu	GGC Gly 245	CTG Leu	CAG Gln	834
CTC Leu	TCG Ser	GTG Val	GAG Glu 250	ACG Thr	CTG Leu	GAT Asp	GGG Gly	CAG Gln 255	AGC Ser	ATC Ile	AAC Asn	CCC Pro	AAG Lys 260	TTG Leu	GCG Ala	882
GGC Gly	CTG Leu	ATT Ile 265	GGG Gly	CGG Arg	CAC His	GGG Gly	CCC Pro 270	CAG Gln	AAC Asn	AAG Lys	CAG Gln	CCC Pro 275	TTC Phe	ATG Met	GTG Val	930
GCT Ala 280	TTC Phe	TTC Phe	AAG Lys	GCC Ala	ACG Thr	GAG Glu 285	GTC Val	CAC His	TTC Phe	CGC Arg	AGC Ser 290	ATC Ile	CGG Arg	TCC Ser	ACG Thr	978
GGG Gly 295	AGC Ser	AAA Lys	CAG Gln	CGC Arg	AGC Ser 300	CAG Gln	AAC Asn	CGC Arg	TCC Ser	AAG Lys 305	ACG Thr	CCC Pro	AAG Lys	AAC Asn	CAG Gln 310	1026

GAA	GCC	CTG	CGG	ATG	GCC	AAC	GTG	GCA	GAG	AAC	AGC	AGC	AGC	GAC	CAG	1074
Glu	Ala	Leu	Arg	Met	Ala	Asn	Val	Ala	Glu	Asn	Ser	Ser	Ser	Asp	Gln	
				315					320					325		
AGG	CAG	GCC	TGT	AAG	AAG	CAC	GAG	CTG	TAT	GTC	AGC	TTC	CGA	GAC	CTG	1122
Arg	Gln	Ala	Cys	Lys	Lys	His	Glu	Leu	Tyr	Val	Ser	Phe	Arg	Asp	Leu	
			330					335					340			
GGC	TGG	CAG	GAC	TGG	ATC	ATC	GCG	CCT	GAA	GGC	TAC	GCC	GCC	TAC	TAC	1170
Gly	Trp	Gln	Asp	Trp	Ile	Ile	Ala	Pro	Glu	Gly	Tyr	Ala	Ala	Tyr	Tyr	
		345					350					355				
TGT	GAG	GGG	GAG	TGT	GCC	TTC	CCT	CTG	AAC	TCC	TAC	ATG	AAC	GCC	ACC	1218
Cys	Glu	Gly	Glu	Cys	Ala	Phe	Pro	Leu	Asn	Ser	Tyr	Met	Asn	Ala	Thr	
	360					365					370					
AAC	CAC	GCC	ATC	GTG	CAG	ACG	CTG	GTC	CAC	TTC	ATC	AAC	CCG	GAA	ACG	1266
Asn	His	Ala	Ile	Val	Gln	Thr	Leu	Val	His	Phe	Ile	Asn	Pro	Glu	Thr	
					380					385					390	
GTG	CCC	AAG	CCC	TGC	TGT	GCG	CCC	ACG	CAG	CTC	AAT	GCC	ATC	TCC	GTC	1314
Val	Pro	Lys	Pro	Cys	Cys	Ala	Pro	Thr	Gln	Leu	Asn	Ala	Ile	Ser	Val	
				395					400					405		
CTC	TAC	TTC	GAT	GAC	AGC	TCC	AAC	GTC	ATC	CTG	AAG	AAA	TAC	AGA	AAC	1362
Leu	Tyr	Phe	Asp	Asp	Ser	Ser	Asn	Val	Ile	Leu	Lys	Lys	Tyr	Arg	Asn	
			410					415					420			
ATG	GTG	GTC	CGG	GCC	TGT	GGC	TGC	CAC	TAGCTCCTCC GAGAATTCAG						1409	
Met	Val	Val	Arg	Ala	Cys	Gly	Cys	His								
		425				430										
ACCCTTTGGG GCCAAGTTTT TCTGGATCCT CCATTGCTC																1448

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	His	Val	Arg	Ser	Leu	Arg	Ala	Ala	Ala	Pro	His	Ser	Phe	Val	Ala
1				5					10					15	
Leu	Trp	Ala	Pro	Leu	Phe	Leu	Leu	Arg	Ser	Ala	Leu	Ala	Asp	Phe	Ser
			20					25					30		
Leu	Asp	Asn	Glu	Val	His	Ser	Ser	Phe	Ile	His	Arg	Arg	Leu	Arg	Ser
		35					40					45			
Gln	Glu	Arg	Arg	Glu	Met	Gln	Arg	Glu	Ile	Leu	Ser	Ile	Leu	Gly	Leu
	50					55					60				
Pro	His	Arg	Pro	Arg	Pro	His	Leu	Gln	Gly	Lys	His	Asn	Ser	Ala	Pro

65					70					75					80				
Met	Phe	Met	Leu	Asp 85	Leu	Tyr	Asn	Ala	Met 90	Ala	Val	Glu	Glu	Gly 95	Gly				
Gly	Pro	Gly	Gly 100	Gln	Gly	Phe	Ser	Tyr 105	Pro	Tyr	Lys	Ala	Val 110	Phe	Ser				
Thr	Gln	Gly 115	Pro	Pro	Leu	Ala	Ser 120	Leu	Gln	Asp	Ser	His 125	Phe	Leu	Thr				
Asp	Ala 130	Asp	Met	Val	Met	Ser 135	Phe	Val	Asn	Leu	Val 140	Glu	His	Asp	Lys				
Glu 145	Phe	Phe	His	Pro	Arg 150	Tyr	His	His	Arg	Glu 155	Phe	Arg	Phe	Asp	Leu 160				
Ser	Lys	Ile	Pro	Glu 165	Gly	Glu	Ala	Val	Thr 170	Ala	Ala	Glu	Phe	Arg 175	Ile				
Tyr	Lys	Asp	Tyr 180	Ile	Arg	Glu	Arg	Phe 185	Asp	Asn	Glu	Thr	Phe 190	Arg	Ile				
Ser	Val	Tyr 195	Gln	Val	Leu	Gln	Glu 200	His	Leu	Gly	Arg	Glu 205	Ser	Asp	Leu				
Phe	Leu 210	Leu	Asp	Ser	Arg	Thr 215	Leu	Trp	Ala	Ser	Glu 220	Glu	Gly	Trp	Leu				
Val 225	Phe	Asp	Ile	Thr	Ala 230	Thr	Ser	Asn	His	Trp 235	Val	Val	Asn	Pro	Arg 240				
His	Asn	Leu	Gly	Leu 245	Gln	Leu	Ser	Val	Glu 250	Thr	Leu	Asp	Gly	Gln 255	Ser				
Ile	Asn	Pro	Lys 260	Leu	Ala	Gly	Leu	Ile 265	Gly	Arg	His	Gly	Pro 270	Gln	Asn				
Lys	Gln	Pro 275	Phe	Met	Val	Ala	Phe 280	Phe	Lys	Ala	Thr	Glu 285	Val	His	Phe				
Arg	Ser 290	Ile	Arg	Ser	Thr	Gly 295	Ser	Lys	Gln	Arg	Ser 300	Gln	Asn	Arg	Ser				
Lys 305	Thr	Pro	Lys	Asn	Gln 310	Glu	Ala	Leu	Arg	Met 315	Ala	Asn	Val	Ala	Glu 320				
Asn	Ser	Ser	Ser	Asp 325	Gln	Arg	Gln	Ala	Cys 330	Lys	Lys	His	Glu	Leu 335	Tyr				
Val	Ser	Phe	Arg 340	Asp	Leu	Gly	Trp	Gln 345	Asp	Trp	Ile	Ile	Ala 350	Pro	Glu				
Gly	Tyr	Ala 355	Ala	Tyr	Tyr	Cys	Glu 360	Gly	Glu	Cys	Ala	Phe 365	Pro	Leu	Asn				
Ser	Tyr 370	Met	Asn	Ala	Thr	Asn 375	His	Ala	Ile	Val	Gln 380	Thr	Leu	Val	His				
Val	Ile	Asn	Pro	Glu	Thr	Val	Pro	Lys	Pro	Cys	Cys	Ala	Pro	Thr	Gln				

Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile

405410415

Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His

420425430

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2923 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (F) TISSUE TYPE: Human placenta
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: Stratagene catalog #936203 Human placenta cDNA library
 - (B) CLONE: BMP6C35
- (viii) POSITION IN GENOME:
 - (C) UNITS: bp
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 160..1701
- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 1282..1698
- (ix) FEATURE:
 - (A) NAME/KEY: mRNA
 - (B) LOCATION: 1..2923

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGACCATGAG AGATAAGGAC TGAGGGCCAG GAAGGGGAAG CGAGCCCGCC GAGAGGTGGC60

GGGGACTGCT CACGCCAAGG GCCACAGCGG CCGCGCTCCG GCCTCGCTCC GCCGCTCCAC120

GCCTCGCGGG ATCCGCGGGG GCAGCCCGGC CGGGCGGGG ATG CCG GGG CTG GGG174

Met Pro Gly Leu Gly-374-370

CGG AGG GCG CAG TGG CTG TGC TGG TGG TGG GGG CTG CTG TGC AGC TGC222

Arg Arg Ala Gln Trp Leu Cys Trp Trp Trp Gly Leu Leu Cys Ser Cys-365-360-355

TGC GGG CCC CCG CCG CTG CGG CCG CCC TTG CCC GCT GCC GCG GCC GCC270

Cys Gly Pro Pro Pro Leu Ala Pro Pro Leu Pro Ala Ala Ala Ala Ala	-350	-345	-340	
GCC GCC GGG GGG CAG CTG CTG GGG GAC GGC GGG AGC CCC GGC CGC ACG				318
Ala Ala Gly Gly Gln Leu Leu Gly Asp Gly Gly Ser Pro Gly Arg Thr	-335	-330	-325	
GAG CAG CCG CCG CCG TCG CCG CAG TCC TCC TCG GGC TTC CTG TAC CGG				366
Glu Gln Pro Pro Pro Ser Pro Gln Ser Ser Ser Gly Phe Leu Tyr Arg	-320	-315	-310	
CGG CTC AAG ACG CAG GAG AAG CGG GAG ATG CAG AAG GAG ATC TTG TCG				414
Arg Leu Lys Thr Gln Glu Lys Arg Glu Met Gln Lys Glu Ile Leu Ser	-305	-300	-295	-290
GTG CTG GGG CTC CCG CAC CGG CCC CGG CCC CTG CAC GGC CTC CAA CAG				462
Val Leu Gly Leu Pro His Arg Pro Arg Pro Leu His Gly Leu Gln Gln	-285		-280	-275
CCG CAG CCC CCG GCG CTC CGG CAG CAG GAG GAG CAG CAG CAG CAG CAG				510
Pro Gln Pro Pro Ala Leu Arg Gln Gln Glu Glu Gln Gln Gln Gln Gln	-270	-265	-260	
CAG CTG CCT CGC GGA GAG CCC CCT CCC GGG CGA CTG AAG TCC GCG CCC				558
Gln Leu Pro Arg Gly Glu Pro Pro Pro Gly Arg Leu Lys Ser Ala Pro	-255	-250	-245	
CTC TTC ATG CTG GAT CTG TAC AAC GCC CTG TCC GCC GAC AAC GAC GAG				606
Leu Phe Met Leu Asp Leu Tyr Asn Ala Leu Ser Ala Asp Asn Asp Glu	-240	-235	-230	
GAC GGG GCG TCG GAG GGG GAG AGG CAG CAG TCC TGG CCC CAC GAA GCA				654
Asp Gly Ala Ser Glu Gly Glu Arg Gln Gln Ser Trp Pro His Glu Ala	-225	-220	-215	-210
GCC AGC TCG TCC CAG CGT CGG CAG CCG CCC CCG GGC GCC GCG CAC CCG				702
Ala Ser Ser Ser Gln Arg Arg Gln Pro Pro Pro Gly Ala Ala His Pro	-205	-200	-195	
CTC AAC CGC AAG AGC CTT CTG GCC CCC GGA TCT GGC AGC GGC GGC GCG				750
Leu Asn Arg Lys Ser Leu Leu Ala Pro Gly Ser Gly Ser Gly Gly Ala	-190	-185	-180	
TCC CCA CTG ACC AGC GCG CAG GAC AGC GCC TTC CTC AAC GAC GCG GAC				798
Ser Pro Leu Thr Ser Ala Gln Asp Ser Ala Phe Leu Asn Asp Ala Asp	-175	-170	-165	
ATG GTC ATG AGC TTT GTG AAC CTG GTG GAG TAC GAC AAG GAG TTC TCC				846
Met Val Met Ser Phe Val Asn Leu Val Glu Tyr Asp Lys Glu Phe Ser	-160	-155	-150	
CCT CGT CAG CGA CAC CAC AAA GAG TTC AAG TTC AAC TTA TCC CAG ATT				894
Pro Arg Gln Arg His His Lys Glu Phe Lys Phe Asn Leu Ser Gln Ile	-145	-140	-135	-130
CCT GAG GGT GAG GTG GTG ACG GCT GCA GAA TTC CGC ATC TAC AAG GAC				942
Pro Glu Gly Glu Val Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp	-125	-120	-115	
TGT GTT ATG GGG AGT TTT AAA AAC CAA ACT TTT CTT ATC AGC ATT TAT				990

Cys	Val	Met	Gly	Ser	Phe	Leu	Asn	Gln	Thr	Phe	Leu	Ile	Ser	Ile	Tyr	
			-110					-105					-100			
CAA	GTC	TTA	CAG	GAG	CAT	CAG	CAC	AGA	GAC	TCT	GAC	CTG	TTT	TTG	TTG	1038
Gln	Val	Leu	Gln	Glu	His	Gln	His	Arg	Asp	Ser	Asp	Leu	Phe	Leu	Leu	
		-95					-90					-85				
GAC	ACC	CGT	GTA	GTA	TGG	GCC	TCA	GAA	GAA	GGC	TGG	CTG	GAA	TTT	GAC	1086
Asp	Thr	Arg	Val	Val	Trp	Ala	Ser	Glu	Glu	Gly	Trp	Leu	Glu	Phe	Asp	
	-80					-75					-70					
ATC	ACG	GCC	ACT	AGC	AAT	CTG	TGG	GTT	GTG	ACT	CCA	CAG	CAT	AAC	ATG	1134
Ile	Thr	Ala	Thr	Ser	Asn	Leu	Trp	Val	Val	Thr	Pro	Gln	His	Asn	Met	
	-65				-60					-55					-50	
GGG	CTT	CAG	CTG	AGC	GTG	GTG	ACA	AGG	GAT	GGA	GTC	CAC	GTC	CAC	CCC	1182
Gly	Leu	Gln	Leu	Ser	Val	Val	Thr	Arg	Asp	Gly	Val	His	Val	His	Pro	
				-45					-40					-35		
CGA	GCC	GCA	GGC	CTG	GTG	GGC	AGA	GAC	GGC	CCT	TAC	GAT	AAG	CAG	CCC	1230
Arg	Ala	Ala	Gly	Leu	Val	Gly	Arg	Asp	Gly	Pro	Tyr	Asp	Lys	Gln	Pro	
			-30					-25					-20			
TTC	ATG	GTG	GCT	TTC	TTC	AAA	GTG	AGT	GAG	GTC	CAC	GTG	CGC	ACC	ACC	1278
Phe	Met	Val	Ala	Phe	Phe	Lys	Val	Ser	Glu	Val	His	Val	Arg	Thr	Thr	
	-15						-10					-5				
AGG	TCA	GCC	TCC	AGC	CGG	CGC	CGA	CAA	CAG	AGT	CGT	AAT	CGC	TCT	ACC	1326
Arg	Ser	Ala	Ser	Ser	Arg	Arg	Arg	Gln	Gln	Ser	Arg	Asn	Arg	Ser	Thr	
	1				5					10					15	
CAG	TCC	CAG	GAC	GTG	GCG	CGG	GTC	TCC	AGT	GCT	TCA	GAT	TAC	AAC	AGC	1374
Gln	Ser	Gln	Asp	Val	Ala	Arg	Val	Ser	Ser	Ala	Ser	Asp	Tyr	Asn	Ser	
				20					25					30		
AGT	GAA	TTG	AAA	ACA	GCC	TGC	AGG	AAG	CAT	GAG	CTG	TAT	GTG	AGT	TTC	1422
Ser	Glu	Leu	Lys	Thr	Ala	Cys	Arg	Lys	His	Glu	Leu	Tyr	Val	Ser	Phe	
			35					40					45			
CAA	GAC	CTG	GGA	TGG	CAG	GAC	TGG	ATC	ATT	GCA	CCC	AAG	GGC	TAT	GCT	1470
Gln	Asp	Leu	Gly	Trp	Gln	Asp	Trp	Ile	Ile	Ala	Pro	Lys	Gly	Tyr	Ala	
		50					55					60				
GCC	AAT	TAC	TGT	GAT	GGA	GAA	TGC	TCC	TTC	CCA	CTC	AAC	GCA	CAC	ATG	1518
Ala	Asn	Tyr	Cys	Asp	Gly	Glu	Cys	Ser	Phe	Pro	Leu	Asn	Ala	His	Met	
	65					70					75					
AAT	GCA	ACC	AAC	CAC	GCG	ATT	GTG	CAG	ACC	TTG	GTT	CAC	CTT	ATG	AAC	1566
Asn	Ala	Thr	Asn	His	Ala	Ile	Val	Gln	Thr	Leu	Val	His	Leu	Met	Asn	
	80				85					90					95	
CCC	GAG	TAT	GTC	CCC	AAA	CCG	TGC	TGT	GCG	CCA	ACT	AAG	CTA	AAT	GCC	1614
Pro	Glu	Tyr	Val	Pro	Lys	Pro	Cys	Cys	Ala	Pro	Thr	Lys	Leu	Asn	Ala	
				100					105					110		
ATC	TCG	GTT	CTT	TAC	TTT	GAT	GAC	AAC	TCC	AAT	GTC	ATT	CTG	AAA	AAA	1662
Ile	Ser	Val	Leu	Tyr	Phe	Asp	Asp	Asn	Ser	Asn	Val	Ile	Leu	Lys	Lys	
			115					120					125			
TAC	AGG	AAT	ATG	GTT	GTA	AGA	GCT	TGT	GGA	TGC	CAC	TAACTCGAAA				1708

Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
130 135

140

CCAGATGCTG	GGGACACACA	TTCTGCCTTG	GATTCCTAGA	TTACATCTGC	CTTAAAAAAA	1768
CACGGAAGCA	CAGTTGGAGG	TGGGACGATG	AGACTTTGAA	ACTATCTCAT	GCCAGTGCCT	1828
TATTACCCAG	GAAGATTTTA	AAGGACCTCA	TTAATAATTT	GCTCACTTGG	TAAATGACGT	1888
GAGTAGTTGT	TGGTCTGTAG	CAAGCTGAGT	TTGGATGTCT	GTAGCATAAG	GTCTGGTAAC	1948
TGCAGAAACA	TAACCGTGAA	GCTCTTCCTA	CCCTCCTCCC	CCAAAAACCC	ACCAAAATTA	2008
GTTTTAGCTG	TAGATCAAGC	TATTTGGGGT	GTTTGTTAGT	AAATAGGGAA	AATAATCTCA	2068
AAGGAGTTAA	ATGTATTCTT	GGCTAAAGGA	TCAGCTGGTT	CAGTACTGTC	TATCAAAGGT	2128
AGATTTTACA	GAGAACAGAA	ATCGGGGAAG	TGGGGGGAAC	GCCTCTGTTC	AGTTCATTCC	2188
CAGAAGTCCA	CAGGACGCAC	AGCCCAGGCC	ACAGCCAGGG	CTCCACGGGG	CGCCCTTGTC	2248
TCAGTCATTG	CTGTTGTATG	TTCGTGCTGG	AGTTTTGTTG	GTGTGAAAAT	ACACTTATTT	2308
CAGCCAAAAC	ATACCATTTC	TACACCTCAA	TCCTCCATTT	GCTGTACTCT	TTGCTAGTAC	2368
CAAAGTAGA	CTGATTACAC	TGAGGTGAGG	CTACAAGGGG	TGTGTAACCG	TGTAACACGT	2428
GAAGGCAGTG	CTCACCTCTT	CTTTACCAGA	ACGGTTCTTT	GACCAGCACA	TTAACTTCTG	2488
GACTGCCGGC	TCTAGTACCT	TTTCAGTAAA	GTGGTTCTCT	GCCTTTTTTAC	TATACAGCAT	2548
ACCACGCCAC	AGGGTTAGAA	CCAACGAAGA	AAATAAAATG	AGGGTGCCCA	GCTTATAAGA	2608
ATGGTGTTAG	GGGGATGAGC	ATGCTGTTTA	TGAACGGAAA	TCATGATTTC	CCTGTAGAAA	2668
GTGAGGCTCA	GATTAAATTT	TAGAATATTT	TCTAAATGTC	TTTTTCACAA	TCATGTGACT	2728
GGGAAGGCAA	TTTCATACTA	AACTGATTAA	ATAATACATT	TATAATCTAC	AACTGTTTGC	2788
ACTTACAGCT	TTTTTTGTAA	ATATAAACTA	TAATTTATTG	TCTATTTTAT	ATCTGTTTTG	2848
CTGTGGCGTT	GGGGGGGGGG	CCGGGCTTTT	GGGGGGGGGG	GTTTGTTTGG	GGGGTGTCGT	2908
GGTGTGGGCG	GGCGG					2923

1828

1888

1948

2008

2068

2128

2188

2248

2308

2368

2428

3488

2548

3608

2668

2728

2799

2848

2008

2022

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 513 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Pro Gly Leu Gly Arg Arg Ala Gln Trp Leu Cys Trp Trp Trp Gly
-374 -370 -365 -360

-370

-365

-360

Leu Leu Cys Ser Cys Cys Gly Pro Pro Pro Leu Arg Pro Pro Leu Pro
 -355 -350 -345

Ala Ala Ala Ala Ala Ala Gly Gly Gln Leu Leu Gly Asp Gly Gly
 -340 -335 -330

Ser Pro Gly Arg Thr Glu Gln Pro Pro Pro Ser Pro Gln Ser Ser Ser
 -325 -320 -315

Gly Phe Leu Tyr Arg Arg Leu Lys Thr Gln Glu Lys Arg Glu Met Gln
 -310 -305 -300 -295

Lys Glu Ile Leu Ser Val Leu Gly Leu Pro His Arg Pro Arg Pro Leu
 -290 -285 -280

His Gly Leu Gln Gln Pro Gln Pro Pro Ala Leu Arg Gln Gln Glu Glu
 -275 -270 -265

Gln Gln Gln Gln Gln Gln Leu Pro Arg Gly Glu Pro Pro Pro Gly Arg
 -260 -255 -250

Leu Lys Ser Ala Pro Leu Phe Met Leu Asp Leu Tyr Asn Ala Leu Ser
 -245 -240 -235

Ala Asp Asn Asp Glu Asp Gly Ala Ser Glu Gly Glu Arg Gln Gln Ser
 -230 -225 -220 -215

Trp Pro His Glu Ala Ala Ser Ser Ser Gln Arg Arg Gln Pro Pro Pro
 -210 -205 -200

Gly Ala Ala His Pro Leu Asn Arg Lys Ser Leu Leu Ala Pro Gly Ser
 -195 -190 -185

Gly Ser Gly Gly Ala Ser Pro Leu Thr Ser Ala Gln Asp Ser Ala Phe
 -180 -175 -170

Leu Asn Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu Tyr
 -165 -160 -155

Asp Lys Glu Phe Ser Pro Arg Gln Arg His His Lys Glu Phe Lys Phe
 -150 -145 -140 -135

Asn Leu Ser Gln Ile Pro Glu Gly Glu Val Val Thr Ala Ala Glu Phe
 -130 -125 -120

Arg Ile Tyr Lys Asp Cys Val Met Gly Ser Phe Lys Asn Gln Thr Phe
 -115 -110 -105

Leu Ile Ser Ile Tyr Gln Val Leu Gln Glu His Gln His Arg Asp Ser
 -100 -95 -90

Asp Leu Phe Leu Leu Asp Thr Arg Val Val Trp Ala Ser Glu Glu Gly
 -85 -80 -75

Trp Leu Glu Phe Asp Ile Thr Ala Thr Ser Asn Leu Trp Val Val Thr
 -70 -65 -60 -55

Pro Gln His Asn Met Gly Leu Gln Leu Ser Val Val Thr Arg Asp Gly
 -50 -45 -40

Val His Val His Pro Arg Ala Ala Gly Leu Val Gly Arg Asp Gly Pro
 -35 -30 -25
 Tyr Asp Lys Gln Pro Phe Met Val Ala Phe Phe Lys Val Ser Glu Val
 -20 -15 -10
 His Val Arg Thr Thr Arg Ser Ala Ser Ser Arg Arg Arg Gln Gln Ser
 -5 1 5 10
 Arg Asn Arg Ser Thr Gln Ser Gln Asp Val Ala Arg Val Ser Ser Ala
 15 20 25
 Ser Asp Tyr Asn Ser Ser Glu Leu Lys Thr Ala Cys Arg Lys His Glu
 30 35 40
 Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala
 45 50 55
 Pro Lys Gly Tyr Ala Ala Asn Tyr Cys Asp Gly Glu Cys Ser Phe Pro
 60 65 70
 Leu Asn Ala His Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu
 75 80 85 90
 Val His Leu Met Asn Pro Glu Tyr Val Pro Lys Pro Cys Cys Ala Pro
 95 100 105
 Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Asn Ser Asn
 110 115 120
 Val Ile Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys
 125 130 135
 His

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2153 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (H) CELL LINE: U2-OS osteosarcoma

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: U2-OS human osteosarcoma cDNA library
- (B) CLONE: U2-16

(viii) POSITION IN GENOME:

- (C) UNITS: bp

(ix) FEATURE:

- (A) NAME/KEY: CDS

(B) LOCATION: 69..2063

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 1647..2060

. (ix) FEATURE:

(A) NAME/KEY: mRNA

(B) LOCATION: 1..2153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTGGTATATT TGTGCCTGCT GGAGGTGGAA TTAACAGTAA GAAGGAGAAA GGGATTGAAT	60
GGACTTACAG GAAGGATTTC AAGTAAATTC AGGGAAACAC ATTTACTTGA ATAGTACAAC	120
CTAGAGTATT ATTTTACACT AAGACGACAC AAAAGATGTT AAAGTTATCA CCAAGCTGCC	180
GGACAGATAT ATATTCCAAC ACCAAGGTGC AGATCAGCAT AGATCTGTGA TTCAGAAATC	240
AGGATTTGTT TTGGAAAGAG CTCAAGGGTT GAGAAGAACT CAAAAGCAAG TGAAGATTAC	300
TTTGGGAACT ACAGTTTATC AGAAGATCAA CTTTGTCTAA TTCAAATACC AAAGGCCTGA	360
TTATCATAAA TTCATATAGG AATGCATAGG TCATCTGATC AAATAATATT AGCCGTCTTC	420
TGCTACATCA ATGCAGCAAA AACTCTTAAC AACTGTGGAT AATTGGAAAT CTGAGTTTCA	480
GCTTTCTTAG AAATAACTAC TCTTGACATA TTCCAAAATA TTTAAAATAG GACAGGAAAA	540
TCGGTGAGGA TGTTGTGCTC AGAAATGTCA CTGTCATGAA AAATAGGTAA ATTTGTTTTT	600
TCAGCTACTG GGAAACTGTA CCTCCTAGAA CCTTAGGTTT TTTTTTTTTT AAGAGGACAA	660
GAAGGACTAA AAATATCAAC TTTTGCTTTT GGACAAAA ATG CAT CTG ACT GTA	713
Met His Leu Thr Val	
-316-315	
TTT TTA CTT AAG GGT ATT GTG GGT TTC CTC TGG AGC TGC TGG GTT CTA	761
Phe Leu Leu Lys Gly Ile Val Gly Phe Leu Trp Ser Cys Trp Val Leu	
-310 -305 -300	
GTG GGT TAT GCA AAA GGA GGT TTG GGA GAC AAT CAT GTT CAC TCC AGT	809
Val Gly Tyr Ala Lys Gly Gly Leu Gly Asp Asn His Val His Ser Ser	
-295 -290 -285 -280	
TTT ATT TAT AGA AGA CTA CGG AAC CAC GAA AGA CGG GAA ATA CAA AGG	857
Phe Ile Tyr Arg Arg Leu Arg Asn His Glu Arg Arg Glu Ile Gln Arg	
-275 -270 -265	
GAA ATT CTC TCT ATC TTG GGT TTG CCT CAC AGA CCC AGA CCA TTT TCA	905
Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg Pro Arg Pro Phe Ser	
-260 -255 -250	
CCT GGA AAA ATG ACC AAT CAA GCG TCC TCT GCA CCT CTC TTT ATG CTG	953
Pro Gly Lys Met Thr Asn Gln Ala Ser Ser Ala Pro Leu Phe Met Leu	
-245 -240 -235	
GAT CTC TAC AAT GCC GAA GAA AAT CCT GAA GAG TCG GAG TAC TCA GTA	1001

Asp -230	Leu	Tyr	Asn	Ala	Glu	Glu	Asn	Pro	Glu	Glu	Ser	Glu	Tyr	Ser	Val	
AGG -215	GCA	TCC	TTG	GCA	GAA	GAG	ACC	AGA	GGG	GCA	AGA	AAG	GGA	TAC	CCA	1049
Arg	Ala	Ser	Leu	Ala	Glu	Glu	Thr	Arg	Gly	Ala	Arg	Lys	Gly	Tyr	Pro	
GCC Ala	TCT Ser	CCC Pro	AAT Asn	GGG Gly	TAT Tyr	CCT Pro	CGT Arg	CGC Arg	ATA Ile	CAG Gln	TTA Leu	TCT Ser	CGG Arg	ACG Thr	ACT Thr	1097
CCT Pro	CTG Leu	ACC Thr	ACC Thr	CAG Gln	AGT Ser	CCT Pro	CCT Pro	CTA Leu	GCC Ala	AGC Ser	CTC Leu	CAT His	GAT Asp	ACC Thr	AAC Asn	1145
TTT Phe	CTG Leu	AAT Asn	GAT Asp	GCT Ala	GAC Asp	ATG Met	GTC Val	ATG Met	AGC Ser	TTT Phe	GTC Val	AAC Asn	TTA Leu	GTT Val	GAA Glu	1193
AGA Arg	GAC Asp	AAG Lys	GAT Asp	TTT Phe	TCT Ser	CAC His	CAG Gln	CGA Arg	AGG Arg	CAT His	TAC Tyr	AAA Lys	GAA Glu	TTT Phe	CGA Arg	1241
TTT Phe	GAT Asp	CTT Leu	ACC Thr	CAA Gln	ATT Ile	CCT Pro	CAT His	GGA Gly	GAG Glu	GCA Ala	GTG Val	ACA Thr	GCA Ala	GCT Ala	GAA Glu	1289
TTC Phe	CGG Arg	ATA Ile	TAC Tyr	AAG Lys	GAC Asp	CGG Arg	AGC Ser	AAC Asn	AAC Asn	CGA Arg	TTT Phe	GAA Glu	AAT Asn	GAA Glu	ACA Thr	1337
ATT Ile	AAG Lys	ATT Ile	AGC Ser	ATA Ile	TAT Tyr	CAA Gln	ATC Ile	ATC Ile	AAG Lys	GAA Glu	TAC Tyr	ACA Thr	AAT Asn	AGG Arg	GAT Asp	1385
GCA Ala	GAT Asp	CTG Leu	TTC Phe	TTG Leu	TTA Leu	GAC Asp	ACA Thr	AGA Arg	AAG Lys	GCC Ala	CAA Gln	GCT Ala	TTA Leu	GAT Asp	GTG Val	1433
GGT Gly	TGG Trp	CTT Leu	GTC Val	TTT Phe	GAT Asp	ATC Ile	ACT Thr	GTG Val	ACC Thr	AGC Ser	AAT Asn	CAT His	TGG Trp	GTG Val	ATT Ile	1481
AAT Asn	CCC Pro	CAG Gln	AAT Asn	AAT Asn	TTG Leu	GGC Gly	TTA Leu	CAG Gln	CTC Leu	TGT Cys	GCA Ala	GAA Glu	ACA Thr	GGG Gly	GAT Asp	1529
GGA Gly	CGC Arg	AGT Ser	ATC Ile	AAC Asn	GTA Val	AAA Lys	TCT Ser	GCT Ala	GGT Gly	CTT Leu	GTG Val	GGA Gly	AGA Arg	CAG Gln	GGA Gly	1577
CCT Pro	CAG Gln	TCA Ser	AAA Lys	CAA Gln	CCA Pro	TTC Phe	ATG Met	GTG Val	GCC Ala	TTC Phe	TTC Phe	AAG Lys	GCG Ala	AGT Ser	GAG Glu	1625
GTA Val	CTT Leu	CTT Leu	CGA Arg	TCC Ser	GTG Val	AGA Arg	GCA Ala	GCC Ala	AAC Asn	AAA Lys	CGA Arg	AAA Lys	AAT Asn	CAA Gln	AAC Asn	1673
CGC	AAT	AAA	TCC	AGC	TCT	CAT	CAG	GAC	TCC	TCC	AGA	ATG	TCC	AGT	GTT	1721

Arg 10	Asn	Lys	Ser	Ser	Ser	His	Gln	Asp	Ser	Ser	Arg	Met	Ser	Ser	Val 25	
					15					20						
GGA	GAT	TAT	AAC	ACA	AGT	GAG	CAA	AAA	CAA	GCC	TGT	AAG	AAG	CAC	GAA	1769
Gly	Asp	Tyr	Asn	Thr	Ser	Glu	Gln	Lys	Gln	Ala	Cys	Lys	Lys	His	Glu	
				30					35					40		
CTC	TAT	GTG	AGC	TTC	CGG	GAT	CTG	GGA	TGG	CAG	GAC	TGG	ATT	ATA	GCA	1817
Leu	Tyr	Val	Ser	Phe	Arg	Asp	Leu	Gly	Trp	Gln	Asp	Trp	Ile	Ile	Ala	
			45					50					55			
CCA	GAA	GGA	TAC	GCT	GCA	TTT	TAT	TGT	GAT	GGA	GAA	TGT	TCT	TTT	CCA	1865
Pro	Glu	Gly	Tyr	Ala	Ala	Phe	Tyr	Cys	Asp	Gly	Glu	Cys	Ser	Phe	Pro	
		60					65					70				
CTT	AAC	GCC	CAT	ATG	AAT	GCC	ACC	AAC	CAC	GCT	ATA	GTT	CAG	ACT	CTG	1913
Leu	Asn	Ala	His	Met	Asn	Ala	Thr	Asn	His	Ala	Ile	Val	Gln	Thr	Leu	
	75					80					85					
GTT	CAT	CTG	ATG	TTT	CCT	GAC	CAC	GTA	CCA	AAG	CCT	TGT	TGT	GCT	CCA	1961
Val	His	Leu	Met	Phe	Pro	Asp	His	Val	Pro	Lys	Pro	Cys	Cys	Ala	Pro	
	90				95					100					105	
ACC	AAA	TTA	AAT	GCC	ATC	TCT	GTT	CTG	TAC	TTT	GAT	GAC	AGC	TCC	AAT	2009
Thr	Lys	Leu	Asn	Ala	Ile	Ser	Val	Leu	Tyr	Phe	Asp	Asp	Ser	Ser	Asn	
				110				115						120		
GTC	ATT	TTG	AAA	AAA	TAT	AGA	AAT	ATG	GTA	GTA	CGC	TCA	TGT	GGC	TGC	2057
Val	Ile	Leu	Lys	Lys	Tyr	Arg	Asn	Met	Val	Val	Arg	Ser	Cys	Gly	Cys	
			125					130					135			
CAC	TAATATTAAA	TAATATTGAT	AATAACAAAA	AGATCTGTAT	TAAGGTTTAT											2110
His																
GGCTGCAATA	AAAAGCATAC	TTTCAGACAA	ACAGAAAAAA	AAA												2153

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	His	Leu	Thr	Val	Phe	Leu	Leu	Lys	Gly	Ile	Val	Gly	Phe	Leu	Trp	
-316	-315					-310						-305				
Ser	Cys	Trp	Val	Leu	Val	Gly	Tyr	Ala	Lys	Gly	Gly	Leu	Gly	Asp	Asn	
-300				-295						-290				-285		
His	Val	His	Ser	Ser	Phe	Ile	Tyr	Arg	Arg	Leu	Arg	Asn	His	Glu	Arg	
			-280					-275					-270			
Arg	Glu	Ile	Gln	Arg	Glu	Ile	Leu	Ser	Ile	Leu	Gly	Leu	Pro	His	Arg	
	-265					-260						-255				

Pro Arg	Pro Phe	Ser Pro	Gly Lys	Met Thr	Asn Gln	Ala Ser	Ser Ser	Ala	
-250			-245			-240			
Pro Leu	Phe Met	Leu Asp	Leu Tyr	Asn Ala	Glu Glu	Asn Pro	Glu Glu		
-235		-230			-225				
Ser Glu	Tyr Ser	Val Arg	Ala Ser	Leu Ala	Glu Glu	Thr Arg	Gly Ala		
-220		-215			-210		-205		
Arg Lys	Gly Tyr	Pro Ala	Ser Pro	Asn Gly	Tyr Pro	Arg Arg	Ile Gln		
		-200		-195			-190		
Leu Ser	Arg Thr	Thr Pro	Leu Thr	Thr Gln	Ser Pro	Pro Leu	Ala Ser		
	-185		-180				-175		
Leu His	Asp Thr	Asn Phe	Leu Asn	Asp Ala	Asp Met	Val Met	Ser Phe		
-170			-165			-160			
Val Asn	Leu Val	Glu Arg	Asp Lys	Asp Phe	Ser His	Gln Arg	Arg His		
-155			-150			-145			
Tyr Lys	Glu Phe	Arg Phe	Asp Leu	Thr Gln	Ile Pro	His Gly	Glu Ala		
-140		-135			-130		-125		
Val Thr	Ala Ala	Glu Phe	Arg Ile	Tyr Lys	Asp Arg	Ser Asn	Asn Arg		
	-120			-115			-110		
Phe Glu	Asn Glu	Thr Ile	Lys Ile	Ser Ile	Tyr Gln	Ile Ile	Lys Glu		
	-105			-100			-95		
Tyr Thr	Asn Arg	Asp Ala	Asp Leu	Phe Leu	Leu Asp	Thr Arg	Lys Ala		
	-90		-85			-80			
Gln Ala	Leu Asp	Val Gly	Trp Leu	Val Phe	Asp Ile	Thr Val	Thr Ser		
-75		-70			-65				
Asn His	Trp Val	Ile Asn	Pro Gln	Asn Asn	Leu Gly	Leu Gln	Leu Cys		
-60		-55			-50		-45		
Ala Glu	Thr Gly	Asp Gly	Arg Ser	Ile Asn	Val Lys	Ser Ala	Gly Leu		
	-40			-35			-30		
Val Gly	Arg Gln	Gly Pro	Gln Ser	Lys Gln	Pro Phe	Met Val	Ala Phe		
	-25		-20			-15			
Phe Lys	Ala Ser	Glu Val	Leu Leu	Arg Ser	Val Arg	Ala Ala	Asn Lys		
	-10		-5			1			
Arg Lys	Asn Gln	Asn Arg	Asn Lys	Ser Ser	Ser His	Gln Asp	Ser Ser		
5		10		15			20		
Arg Met	Ser Ser	Val Gly	Asp Tyr	Asn Thr	Ser Glu	Gln Lys	Gln Ala		
		25		30			35		
Cys Lys	Lys His	Glu Leu	Tyr Val	Ser Phe	Arg Asp	Leu Gly	Trp Gln		
	40			45		50			
Asp Trp	Ile Ile	Ala Pro	Glu Gly	Tyr Ala	Ala Phe	Tyr Cys	Asp Gly		
	55		60			65			

Glu Cys Ser Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His Ala
 70 75 80
 Ile Val Gln Thr Leu Val His Leu Met Phe Pro Asp His Val Pro Lys
 85 90 95 100
 Pro Cys Cys Ala Pro Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe
 105 110 115
 Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val Val
 120 125 130
 Arg Ser Cys Gly Cys His
 135

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1003 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
 - (F) TISSUE TYPE: Human Heart
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: Human heart cDNA library stratagene catalog
#936208
 - (B) CLONE: hH38
- (viii) POSITION IN GENOME:
 - (C) UNITS: bp
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 8..850
- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 427..843
- (ix) FEATURE:
 - (A) NAME/KEY: mRNA
 - (B) LOCATION: 1..997
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAATTCC GAG CCC CAT TGG AAG GAG TTC CGC TTT GAC CTG ACC CAG ATC
 Glu Pro His Trp Lys Glu Phe Arg Phe Asp Leu Thr Gln Ile
 -139 -135 -130

CCG	GCT	GGG	GAG	GCG	GTC	ACG	GCT	GCG	GAG	TTC	CGG	ATT	TTC	AAG	GTG	97
Pro	Ala	Gly	Glu	Ala	Val	Thr	Ala	Ala	Glu	Phe	Arg	Ile	Tyr	Lys	Val	
-125					-120					-115					-110	
CCC	AGC	ATC	CAC	CTG	CTC	AAC	AGG	ACC	CTC	CAC	GTC	AGC	ATG	TTC	CAG	145
Pro	Ser	Ile	His	Leu	Leu	Asn	Arg	Thr	Leu	His	Val	Ser	Met	Phe	Gln	
				-105					-100					-95		
GTG	GTC	CAG	GAG	CAG	TCC	AAC	AGG	GAG	TCT	GAC	TTG	TTC	TTT	TTG	GAT	193
Val	Val	Gln	Glu	Gln	Ser	Asn	Arg	Glu	Ser	Asp	Leu	Phe	Phe	Leu	Asp	
			-90					-85					-80			
CTT	CAG	ACG	CTC	CGA	GCT	GGA	GAC	GAG	GGC	TGG	CTG	GTG	CTG	GAT	GTC	241
Leu	Gln	Thr	Leu	Arg	Ala	Gly	Asp	Glu	Gly	Trp	Leu	Val	Leu	Asp	Val	
		-75					-70					-65				
ACA	GCA	GCC	AGT	GAC	TGC	TGG	TTG	CTG	AAG	CGT	CAC	AAG	GAC	CTG	GGA	289
Thr	Ala	Ala	Ser	Asp	Cys	Trp	Leu	Leu	Lys	Arg	His	Lys	Asp	Leu	Gly	
	-60					-55					-50					
CTC	CGC	CTC	TAT	GTG	GAG	ACT	GAG	GAT	GGG	CAC	AGC	GTG	GAT	CCT	GGC	337
Leu	Arg	Leu	Tyr	Val	Glu	Thr	Glu	Asp	Gly	His	Ser	Val	Asp	Pro	Gly	
-45					-40					-35					-30	
CTG	GCC	GGC	CTG	CTG	GGT	CAA	CGG	GCC	CCA	CGC	TCC	CAA	CAG	CCT	TTC	385
Leu	Ala	Gly	Leu	Leu	Gly	Gln	Arg	Ala	Pro	Arg	Ser	Gln	Gln	Pro	Phe	
				-25					-20					-15		
GTG	GTC	ACT	TTC	TTC	AGG	GCC	AGT	CCG	AGT	CCC	ATC	CGC	ACC	CCT	CGG	433
Val	Val	Thr	Phe	Phe	Arg	Ala	Ser	Pro	Ser	Pro	Ile	Arg	Thr	Pro	Arg	
			-10					-5					1			
GCA	GTG	AGG	CCA	CTG	AGG	AGG	AGG	CAG	CCG	AAG	AAA	AGC	AAC	GAG	CTG	481
Ala	Val	Arg	Pro	Leu	Arg	Arg	Arg	Gln	Pro	Lys	Lys	Ser	Asn	Glu	Leu	
	5					10					15					
CCG	CAG	GCC	AAC	CGA	CTC	CCA	GGG	ATC	TTT	GAT	GAC	GTC	CAC	GGC	TCC	529
Pro	Gln	Ala	Asn	Arg	Leu	Pro	Gly	Ile	Phe	Asp	Asp	Val	His	Gly	Ser	
20					25					30					35	
CAC	GGC	CGG	CAG	GTC	TGC	CGT	CGG	CAC	GAG	CTC	TAC	GTC	AGC	TTC	CAG	577
His	Gly	Arg	Gln	Val	Cys	Arg	Arg	His	Glu	Leu	Tyr	Val	Ser	Phe	Gln	
				40					45					50		
GAC	CTT	GGC	TGG	CTG	GAC	TGG	GTC	ATC	GCC	CCC	CAA	GGC	TAC	TCA	GCC	625
Asp	Leu	Gly	Trp	Leu	Asp	Trp	Val	Ile	Ala	Pro	Gln	Gly	Tyr	Ser	Ala	
			55					60					65			
TAT	TAC	TGT	GAG	GGG	GAG	TGC	TCC	TTC	CCG	CTG	GAC	TCC	TGC	ATG	AAC	673
Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ser	Phe	Pro	Leu	Asp	Ser	Cys	Met	Asn	
		70					75					80				
GCC	ACC	AAC	CAC	GCC	ATC	CTG	CAG	TCC	CTG	GTG	CAC	CTG	ATG	AAG	CCA	721
Ala	Thr	Asn	His	Ala	Ile	Leu	Gln	Ser	Leu	Val	His	Leu	Met	Lys	Pro	
	85					90					95					
AAC	GCA	GTC	CCC	AAG	GCG	TGC	TGT	GCA	CCC	ACC	AAG	CTG	AGC	GCC	ACC	769
Asn	Ala	Val	Pro	Lys	Ala	Cys	Cys	Ala	Pro	Thr	Lys	Leu	Ser	Ala	Thr	
100					105					110					115	

TCT GTG CTC TAC TAT GAC ACC AGC AAC AAC GTC ATC CTG CCG AAG CAC	817
Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His	
120 125 130	
CGC AAC ATG GTG GTC AAG GCC TGC GGC TGC CAC TGAGTCAGCC CGCCCAGCCC	870
Arg Asn Met Val Val Lys Ala Cys Gly Cys His	
135 140	
TACTGCAGCC ACCCTTCTCA TCTGGATCGG GCCCTGCAGA GGCAGAAAAC CCTTAAATGC	930
TGTCACAGCT CAAGCAGGAG TGTCAGGGGC CCTCACTCTC GGTGCCTACT TCCTGTCAGG	990
CTTCTGGGAA TTC	1003

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Glu Pro His Trp Lys Glu Phe Arg Phe Asp Leu Thr Gln Ile Pro Ala	
-139 -135 -130 -125	
Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Val Pro Ser	
-120 -115 -110	
Ile His Leu Leu Asn Arg Thr Leu His Val Ser Met Phe Gln Val Val	
-105 -100 -95	
Gln Glu Gln Ser Asn Arg Glu Ser Asp Leu Phe Phe Leu Asp Leu Gln	
-90 -85 -80	
Thr Leu Arg Ala Gly Asp Glu Gly Trp Leu Val Leu Asp Val Thr Ala	
-75 -70 -65 -60	
Ala Ser Asp Cys Trp Leu Leu Lys Arg His Lys Asp Leu Gly Leu Arg	
-55 -50 -45	
Leu Tyr Val Glu Thr Glu Asp Gly His Ser Val Asp Pro Gly Leu Ala	
-40 -35 -30	
Gly Leu Leu Gly Gln Arg Ala Pro Arg Ser Gln Gln Pro Phe Val Val	
-25 -20 -15	
Thr Phe Phe Arg Ala Ser Pro Ser Pro Ile Arg Thr Pro Arg Ala Val	
-10 -5 1 5	
Arg Pro Leu Arg Arg Arg Gln Pro Lys Lys Ser Asn Glu Leu Pro Gln	
10 15 20	
Ala Asn Arg Leu Pro Gly Ile Phe Asp Asp Val His Gly Ser His Gly	
25 30 35	
Arg Gln Val Cys Arg Arg His Glu Leu Tyr Val Ser Phe Gln Asp Leu	

Gly Trp Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr
 55 60 65
 Cys Glu Gly Glu Cys Ser Phe Pro Leu Asp Ser Cys Met Asn Ala Thr
 70 75 80 85
 Asn His Ala Ile Leu Gln Ser Leu Val His Leu Met Lys Pro Asn Ala
 90 95 100
 Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr Ser Val
 105 110 115
 Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His Arg Asn
 120 125 130
 Met Val Val Lys Ala Cys Gly Cys His
 135 140

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3623 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: pALBP2-781

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2724..3071

(ix) FEATURE:

- (A) NAME/KEY: terminator
- (B) LOCATION: 3150..3218

(ix) FEATURE:

- (A) NAME/KEY: RBS
- (B) LOCATION: 2222..2723

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GACGAAAGGG CCTCGTGATA CGCCTATTTT TATAGGTAA TGTCATGATA ATAATGGTTT	60
CTTAGACGTC AGGTGGCACT TTTCGGGGAA ATGTGCGCGG AACCCCTATT TGTTTATTTT	120
TCTAAATACA TTCAAATATG TATCCGCTCA TGAGACAATA ACCCTGATAA ATGCTTCAAT	180
AATATTGAAA AAGGAAGAGT ATGAGTATTC AACATTTCCG TGTCGCCCTT ATTCCCTTTT	240
TTGCGGCATT TTGCCTTCCT GTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG	300
CTGAAGATCA GTTGGGTGCA CGAGTGGGT ACATCGAACT GGATCTCAAC AGCGGTAAGA	360

TCCTTGAGAG	TTTTCGCCCC	GAAGAACGTT	TTCCAATGAT	GAGCACTTTT	AAAGTTCTGC	420
TATGTGGCGC	GGTATTATCC	CGTATTGACG	CCGGGCAAGA	GCAACTCGGT	CGCCGCATAC	480
ACTATTCTCA	GAATGACTTG	GTTGAGTACT	CACCAGTCAC	AGAAAAGCAT	CTTACGGATG	540
GCATGACAGT	AAGAGAATTA	TGCAGTGCTG	CCATAACCAT	GAGTGATAAC	ACTGCGGCCA	600
ACTTACTTCT	GACAACGATC	GGAGGACCGA	AGGAGCTAAC	CGCTTTTTTG	CACAACATGG	660
GGGATCATGT	AACTCGCCTT	GATCGTTGGG	AACCGGAGCT	GAATGAAGCC	ATACCAAACG	720
ACGAGCGTGA	CACCACGATG	CCTGTAGCAA	TGGCAACAAC	GTTGCGCAAA	CTATTAAGTG	780
GCGAACTACT	TACTCTAGCT	TCCCGGCAAC	AATTAATAGA	CTGGATGGAG	GCGGATAAAG	840
TTGCAGGACC	ACTTCTGCGC	TCGGCCCTTC	CGGCTGGCTG	GTTTATTGCT	GATAAATCTG	900
GAGCCGGTGA	GCGTGGGTCT	CGCGGTATCA	TTGCAGCACT	GGGGCCAGAT	GGTAAGCCCT	960
CCCGTATCGT	AGTTATCTAC	ACGACGGGGA	GTCAGGCAAC	TATGGATGAA	CGAAATAGAC	1020
AGATCGCTGA	GATAGGTGCC	TCACTGATTA	AGCATTGGTA	ACTGTCAGAC	CAAGTTTACT	1080
CATATATACT	TTAGATTGAT	TTAAAACTTC	ATTTTTAATT	TAAAAGGATC	TAGGTGAAGA	1140
TCCTTTTTGA	TAATCTCATG	ACCAAAATCC	CTTAACGTGA	GTTTTCGTTC	CACTGAGCGT	1200
CAGACCCCGT	AGAAAAGATC	AAAGGATCTT	CTTGAGATCC	TTTTTTTTCTG	CGCGTAATCT	1260
GCTGCTTGCA	AACAAAAAAA	CCACCGCTAC	CAGCGGTGGT	TTGTTTGCCG	GATCAAGAGC	1320
TACCAACTCT	TTTTCCGAAG	GTAAGTGGCT	TCAGCAGAGC	GCAGATACCA	AATACTGTCC	1380
TTCTAGTGTA	GCCGTAGTTA	GGCCACCACT	TCAAGAACTC	TGTAGCACCG	CCTACATACC	1440
TCGCTCTGCT	AATCCTGTTA	CCAGTGGCTG	CTGCCAGTGG	CGATAAGTCG	TGTCTTACCG	1500
GGTTGGACTC	AAGACGATAG	TTACCGGATA	AGGCGCAGCG	GTCGGGCTGA	ACGGGGGGTT	1560
CGTGACACACA	GCCCAGCTTG	GAGCGAACGA	CCTACACCGA	ACTGAGATAC	CTACAGCGTG	1620
AGCATTGAGA	AAGCGCCACG	CTTCCCGAAG	GGAGAAAGGC	GGACAGGTAT	CCGGTAAGCG	1680
GCAGGGTCGG	AACAGGAGAG	CGCACGAGGG	AGCTTCCAGG	GGGAAACGCC	TGGTATCTTT	1740
ATAGTCCTGT	CGGGTTTCGC	CACCTCTGAC	TTGAGCGTCG	ATTTTTGTGA	TGCTCGTCAG	1800
GGGGGCGGAG	CCTATGGAAA	AACGCCAGCA	ACGCGGCCTT	TTTACGGTTC	CTGGCCTTTT	1860
GCTGGCCTTT	TGCTCACATG	TTCTTTCCTG	CGTTATCCCC	TGATTCTGTG	GATAACCGTA	1920
TTACCGCCTT	TGAGTGAGCT	GATACCGCTC	GCCGCAGCCG	AACGACCGAG	CGCAGCGAGT	1980
CAGTGAGCGA	GGAAGCGGAA	GAGCGCCCAA	TACGCAAACC	GCCTCTCCCC	GCGCGTTGGC	2040
CGATTCATTA	ATGCAGAATT	GATCTCTCAC	CTACCAAACA	ATGCCCCCCT	GCAAAAAATA	2100
AATTCATATA	AAAAACATAC	AGATAACCAT	CTGCGGTGAT	AAATTATCTC	TGGCGGTGTT	2160

GACATAAATA CCACTGGCGG TGATACTGAG CACATCAGCA GGACGCACTG ACCACCATGA	2220
AGGTGACGCT CTTAAAAATT AAGCCCTGAA GAAGGGCAGC ATTCAAAGCA GAAGGCTTTG	2280
GGGTGTGTGA TACGAAACGA AGCATTGGCC GTAAGTGCGA TTCCGGATTA GCTGCCAATG	2340
TGCCAATCGC GGGGGGTTTT CGTTCAGGAC TACAACTGCC ACACACCACC AAAGCTAACT	2400
GACAGGAGAA TCCAGATGGA TGCACAAACA CGCCGCCGCG AACGTCGCGC AGAGAAACAG	2460
GCTCAATGGA AAGCAGCAAA TCCCCTGTTG GTTGGGGTAA GCGCAAAACC AGTTCCGAAA	2520
GATTTTTTTTA ACTATAAACG CTGATGGAAG CGTTTATGCG GAAGAGGTAA AGCCCTTCCC	2580
GAGTAACAAA AAAACAACAG CATAAATAAC CCCGCTCTTA CACATTCCAG CCCTGAAAAA	2640
GGGCATCAAA TTAAACCACA CCTATGGTGT ATGCATTTAT TTGCATACAT TCAATCAATT	2700
GTTATCTAAG GAAATACTTA CAT ATG CAA GCT AAA CAT AAA CAA CGT AAA	2750
Met Gln Ala Lys His Lys Gln Arg Lys	
1 5	
CGT CTG AAA TCT AGC TGT AAG AGA CAC CCT TTG TAC GTG GAC TTC AGT	2798
Arg Leu Lys Ser Ser Cys Lys Arg His Pro Leu Tyr Val Asp Phe Ser	
10 15 20 25	
GAC GTG GGG TGG AAT GAC TGG ATT GTG GCT CCC CCG GGG TAT CAC GCC	2846
Asp Val Gly Trp Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr His Ala	
30 35 40	
TTT TAC TGC CAC GGA GAA TGC CCT TTT CCT CTG GCT GAT CAT CTG AAC	2894
Phe Tyr Cys His Gly Glu Cys Pro Phe Pro Leu Ala Asp His Leu Asn	
45 50 55	
TCC ACT AAT CAT GCC ATT GTT CAG ACG TTG GTC AAC TCT GTT AAC TCT	2942
Ser Thr Asn His Ala Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser	
60 65 70	
AAG ATT CCT AAG GCA TGC TGT GTC CCG ACA GAA CTC AGT GCT ATC TCG	2990
Lys Ile Pro Lys Ala Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser	
75 80 85	
ATG CTG TAC CTT GAC GAG AAT GAA AAG GTT GTA TTA AAG AAC TAT CAG	3038
Met Leu Tyr Leu Asp Glu Asn Glu Lys Val Val Leu Lys Asn Tyr Gln	
90 95 100 105	
GAC ATG GTT GTG GAG GGT TGT GGG TGT CGC TAGTACAGCA AAATTAAATA	3088
Asp Met Val Val Glu Gly Cys Gly Cys Arg	
110 115	
CATAAATATA TATATATATA TATATTTTAG AAAAAAGAAA AAAATCTAGA GTCGACCTGC	3148
AGTAATCGTA CAGGGTAGTA CAAATAAAAA AGGCACGTCA GATGACGTGC CTTTTTCTT	3208
GTGAGCAGTA AGCTTGGCAC TGGCCGTCGT TTTACAACGT CGTGACTGGG AAAACCCTGG	3268
CGTTACCCAA CTTAATCGCC TTGCAGCACA TCCCCCTTTC GCCAGCTGGC GTAATAGCGA	3328
AGAGGCCCGC ACCGATCGCC CTTCCCAACA GTTGCGCAGC CTGAATGGCG AATGGCGCCT	3388

GATGCGGTAT TTTCTCCTTA CGCATCTGTG CGGTATTTCA CACCGCATAT ATGGTGCACT	3448
CTCAGTACAA TCTGCTCTGA TGCCGCATAG TTAAGCCAGC CCCGACACCC GCCAACACCC	3508
GCTGACGCGC CCTGACGGGC TTGTCTGCTC CCGGCATCCG CTTACAGACA AGCTGTGACC	3568
GTCTCCGGGA GCTGCATGTG TCAGAGGTTT TCACCGTCAT CACCGAAACG CGCGA	3623

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Gln	Ala	Lys	His	Lys	Gln	Arg	Lys	Arg	Leu	Lys	Ser	Ser	Cys	Lys	
1				5					10					15		
Arg	His	Pro	Leu	Tyr	Val	Asp	Phe	Ser	Asp	Val	Gly	Trp	Asn	Asp	Trp	
			20					25					30			
Ile	Val	Ala	Pro	Pro	Gly	Tyr	His	Ala	Phe	Tyr	Cys	His	Gly	Glu	Cys	
		35				40						45				
Pro	Phe	Pro	Leu	Ala	Asp	His	Leu	Asn	Ser	Thr	Asn	His	Ala	Ile	Val	
	50					55					60					
Gln	Thr	Leu	Val	Asn	Ser	Val	Asn	Ser	Lys	Ile	Pro	Lys	Ala	Cys	Cys	
65				70					75					80		
Val	Pro	Thr	Glu	Leu	Ser	Ala	Ile	Ser	Met	Leu	Tyr	Leu	Asp	Glu	Asn	
			85					90						95		
Glu	Lys	Val	Val	Leu	Lys	Asn	Tyr	Gln	Asp	Met	Val	Val	Glu	Gly	Cys	
		100					105						110			
Gly	Cys	Arg														
		115														

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GAGGGTTGTG GGTGTCGCTA GTGAGTCGAC TACAGCAAAT T

41

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GGATGTGGGT GCCGCTGACT CTAGAGTCGA CGGAATTC

38

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

AATTCACCAT GATTCCTGGT AACCGAATGC T

31

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GTGGTACTAA GGACCATTGG CTTAC

25

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CGACCTGCAG CCATGCATCT GACTGTA

27

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TGCCTGCAGT TTAATATTAG TGGCAGC

27

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CGACCTGCAG CCACC

15

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 81 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TCGACCCACC ATGCCGGGGC TGGGGCGGAG GGCGCAGTGG CTGTGCTGGT GGTGGGGGCT 60
GTGCTGCAGC TGCTGCGGGC C 81

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CGCAGCAGCT GCACAGCAGC CCCCACCACC AGCACAGCCA CTGCGCCCTC CGCCCCAGCC 60
CCGGCATGGT GGG 73

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TCGACTGGTT T 11

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TCGACAGGCT CGCCTGCA

18

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GTCCGAGCGG

10

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CAGGTCGACC CACCATGCAC GTGCGCTCA

29

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

27

TCTGTCGACC TCGGAGGAGC TAGTGGC

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1794 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: bmp-3

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 321..1136

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

AGATCTTGAA AACACCCGGG CCACACACGC CGCGACCTAC AGCTCTTTCT CAGCGTTGGA	60
GTGGAGACGG CGCCCGCAGC GCCCTGCGCG GGTGAGGTCC GCGCAGCTGC TGGGGAAGAG	120
CCCACCTGTC AGGCTGCGCT GGGTCAGCGC AGCAAGTGGG GCTGGCCGCT ATCTCGCTGC	180
ACCCGGCCGC GTCCCGGGCT CCGTGCGCCC TCGCCCCAGC TGGTTTGGAG TTCAACCCTC	240
GGCTCCGCCG CCGGCTCCTT GCGCCTTCGG AGTGTCCTCG AGCGACGCCG GGAGCCGACG	300
CGCCGCGCGG GTACCTAGCC ATG GCT GGG GCG AGC AGG CTG CTC TTT CTG	350
Met Ala Gly Ala Ser Arg Leu Leu Phe Leu	
1 5 10	
TGG CTG GGC TGC TTC TGC GTG AGC CTG GCG CAG GGA GAG AGA CCG AAG	398
Trp Leu Gly Cys Phe Cys Val Ser Leu Ala Gln Gly Glu Arg Pro Lys	
15 20 25	
CCA CCT TTC CCG GAG CTC CGC AAA GCT GTG CCA GGT GAC CGC ACG GCA	446
Pro Pro Phe Pro Glu Leu Arg Lys Ala Val Pro Gly Asp Arg Thr Ala	
30 35 40	
GGT GGT GGC CCG GAC TCC GAG CTG CAG CCG CAA GAC AAG GTC TCT GAA	494
Gly Gly Gly Pro Asp Ser Glu Leu Gln Pro Gln Asp Lys Val Ser Glu	
45 50 55	
CAC ATG CTG CGG CTC TAT GAC AGG TAC AGC ACG GTC CAG GCG GCC CGG	542
His Met Leu Arg Leu Tyr Asp Arg Tyr Ser Thr Val Gln Ala Ala Arg	
60 65 70	
ACA CCG GGC TCC CTG GAG GGA GGC TCG CAG CCC TGG CGC CCT CGG CTC	590
Thr Pro Gly Ser Leu Glu Gly Gly Ser Gln Pro Trp Arg Pro Arg Leu	
75 80 85 90	
CTG CGC GAA GGC AAC ACG GTT CGC AGC TTT CGG GCG GCA GCA GCA GAA	638

Leu	Arg	Glu	Gly	Asn	Thr	Val	Arg	Ser	Phe	Arg	Ala	Ala	Ala	Ala	Glu	
				95					100						105	
ACT	CTT	GAA	AGA	AAA	GGA	CTG	TAT	ATC	TTC	AAT	CTG	ACA	TCG	CTA	ACC	686
Thr	Leu	Glu	Arg	Lys	Gly	Leu	Tyr	Ile	Phe	Asn	Leu	Thr	Ser	Leu	Thr	
			110					115					120			
AAG	TCT	GAA	AAC	ATT	TTG	TCT	GCC	ACA	CTG	TAT	TTC	TGT	ATT	GGA	GAG	734
Lys	Ser	Glu	Asn	Ile	Leu	Ser	Ala	Thr	Leu	Tyr	Phe	Cys	Ile	Gly	Glu	
			125				130					135				
CTA	GGA	AAC	ATC	AGC	CTG	AGT	TGT	CCA	GTG	TCT	GGA	GGA	TGC	TCC	CAT	782
Leu	Gly	Asn	Ile	Ser	Leu	Ser	Cys	Pro	Val	Ser	Gly	Gly	Cys	Ser	His	
	140					145					150					
CAT	GCT	CAG	AGG	AAA	CAC	ATT	CAG	ATT	GAT	CTT	TCT	GCA	TGG	ACC	CTC	830
His	Ala	Gln	Arg	Lys	His	Ile	Gln	Ile	Asp	Leu	Ser	Ala	Trp	Thr	Leu	
155					160				165						170	
AAA	TTC	AGC	AGA	AAC	CAA	AGT	CAA	CTC	CTT	GGC	CAT	CTG	TCA	GTG	GAT	878
Lys	Phe	Ser	Arg	Asn	Gln	Ser	Gln	Leu	Leu	Gly	His	Leu	Ser	Val	Asp	
				175				180						185		
ATG	GCC	AAA	TCT	CAT	CGA	GAT	ATT	ATG	TCC	TGG	CTG	TCT	AAA	GAT	ATC	926
Met	Ala	Lys	Ser	His	Arg	Asp	Ile	Met	Ser	Trp	Leu	Ser	Lys	Asp	Ile	
			190					195					200			
ACT	CAA	TTC	TTG	AGG	AAG	GCC	AAA	GAA	AAT	GAA	GAG	TTC	CTC	ATA	GGA	974
Thr	Gln	Phe	Leu	Arg	Lys	Ala	Lys	Glu	Asn	Glu	Glu	Phe	Leu	Ile	Gly	
		205					210					215				
TTT	AAC	ATT	ACG	TCC	AAG	GGA	CGC	CAG	CTG	CCA	AAG	AGG	AGG	TTA	CCT	1022
Phe	Asn	Ile	Thr	Ser	Lys	Gly	Arg	Gln	Leu	Pro	Lys	Arg	Arg	Leu	Pro	
	220					225					230					
TTT	CCA	GAG	CCT	TAT	ATC	TTG	GTA	TAT	GCC	AAT	GAT	GCC	GCC	ATT	TCT	1070
Phe	Pro	Glu	Pro	Tyr	Ile	Leu	Val	Tyr	Ala	Asn	Asp	Ala	Ala	Ile	Ser	
235					240				245						250	
GAG	CCA	GAA	AGT	GTG	GTA	TCA	AGC	TTA	CAG	GGA	CAC	CGG	AAT	TTT	CCC	1118
Glu	Pro	Glu	Ser	Val	Val	Ser	Ser	Leu	Gln	Gly	His	Arg	Asn	Phe	Pro	
				255					260					265		
ACT	GGA	ACT	GTT	CCC	AAA	TGGG	ATAGCC	ACATCAGAGC	TGCCCTTTCC							1166
Thr	Gly	Thr	Val	Pro	Lys											
			270													
ATTGAGCGGA	GGAAGAAGCG	CTCTACTGGG	GTCTTGCTGC	CTCTGCAGAA	CAACGAGCTT											1226
CCTGGGGCAG	AATACCAGTA	TAAAAAGGAT	GAGGTGTGGG	AGGAGAGAAA	GCCTTACAAG											1286
ACCCTTCAGG	CTCAGGCCCC	TGAAAAGAGT	AAGAATAAAA	AGAAACAGAG	AAAGGGGCCT											1346
CATCGGAAGA	GCCAGACGCT	CCAATTTGAT	GAGCAGACCC	TGAAAAAGGC	AAGGAGAAAG											1406
CAGTGGATTG	AACCTCGGAA	TTGCGCCAGG														

GTGAGAGCTG TGGGGGTCGT TCCTGGGATT CCTGAGCCTT GCTGTGTACC AGAAAAGATG	1646
TCCTCACTCA GTATTTTATT CTTTGATGAA AATAAGAATG TAGTGCTTAA AGTATACCCT	1706
AAATGACAG TAGAGTCTTG CGCTTGCAGA TAACCTGGCA AAGAACTCAT TTGAATGCTT	1766
AATTCAATCT CTAGAGTCGA CGGAATTC	1794

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met	Ala	Gly	Ala	Ser	Arg	Leu	Leu	Phe	Leu	Trp	Leu	Gly	Cys	Phe	Cys	
1				5					10					15		
Val	Ser	Leu	Ala	Gln	Gly	Glu	Arg	Pro	Lys	Pro	Pro	Phe	Pro	Glu	Leu	
			20					25					30			
Arg	Lys	Ala	Val	Pro	Gly	Asp	Arg	Thr	Ala	Gly	Gly	Gly	Pro	Asp	Ser	
		35					40					45				
Glu	Leu	Gln	Pro	Gln	Asp	Lys	Val	Ser	Glu	His	Met	Leu	Arg	Leu	Tyr	
	50					55					60					
Asp	Arg	Tyr	Ser	Thr	Val	Gln	Ala	Ala	Arg	Thr	Pro	Gly	Ser	Leu	Glu	
65					70					75					80	
Gly	Gly	Ser	Gln	Pro	Trp	Arg	Pro	Arg	Leu	Leu	Arg	Glu	Gly	Asn	Thr	
				85					90					95		
Val	Arg	Ser	Phe	Arg	Ala	Ala	Ala	Ala	Glu	Thr	Leu	Glu	Arg	Lys	Gly	
			100					105					110			
Leu	Tyr	Ile	Phe	Asn	Leu	Thr	Ser	Leu	Thr	Lys	Ser	Glu	Asn	Ile	Leu	
		115					120					125				
Ser	Ala	Thr	Leu	Tyr	Phe	Cys	Ile	Gly	Glu	Leu	Gly	Asn	Ile	Ser	Leu	
			130			135					140					
Ser	Cys	Pro	Val	Ser	Gly	Gly	Cys	Ser	His	His	Ala	Gln	Arg	Lys	His	
145					150				155					160		
Ile	Gln	Ile	Asp	Leu	Ser	Ala	Trp	Thr	Leu	Lys	Phe	Ser	Arg	Asn	Gln	
			165					170						175		
Ser	Gln	Leu	Leu	Gly	His	Leu	Ser	Val	Asp	Met	Ala	Lys	Ser	His	Arg	
			180					185					190			
Asp	Ile	Met	Ser	Trp	Leu	Ser	Lys	Asp	Ile	Thr	Gln	Phe	Leu	Arg	Lys	
		195					200					205				

Ala Lys Glu Asn Glu Glu Phe Leu Ile Gly Phe Asn Ile Thr Ser Lys
 210 215 220

Gly Arg Gln Leu Pro Lys Arg Arg Leu Pro Phe Pro Glu Pro Tyr Ile
 225 230 235 240

Leu Val Tyr Ala Asn Asp Ala Ala Ile Ser Glu Pro Glu Ser Val Val
 245 250 255

Ser Ser Leu Gln Gly His Arg Asn Phe Pro Thr Gly Thr Val Pro Lys
 260 265 270

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ATGTCTCATA ATCGTTCTAA AACTCCAAAA AATCAAGAAG CTCTGCGTAT GGCCAACGTG	60
GCAGAGAACA GCAGCAGCGA CCAGAGGCAG GCCTGTAAGA AGCACGAGCT GTATGTCAGC	120
TTCCGAGACC TGGGCTGGCA GGACTGGATC ATCGCGCCTG AAGGCTACGC CGCCTACTAC	180
TGTGAGGGGG AGTGTGCCTT CCCTCTGAAC TCCTACATGA ACGCCACCAA CCACGCCATC	240
GTGCAGACGC TGGTCCACTT CATCAACCCG GAAACGGTGC CCAAGCCCTG CTGTGCGCCC	300
ACGCAGCTCA ATGCCATCTC CGTCCTCTAC TTCGATGACA GCTCCAACGT CATCCTGAAG	360
AAATACAGAA ACATGGTGGT CCGGGCCTGT GGCTGCCACT AGCTCCTCCG AGAATTCAGA	420
CCCTTTGGGG CCAAGTTTTT CTGGATCCT	449

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CAAGAAGGAG ATATACAT

18

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 377 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ATGCGTAAAC AATGGATTGA ACCACGTAAC TGTGCTCGTC GTTATCTGAA AGTAGACTTT	60
GCAGATATTG GCTGGAGTGA ATGGATTATC TCCCCCAAGT CCTTTGATGC CTATTATTGC	120
TCTGGAGCAT GCCAGTTCCC CATGCCAAAG TCTTTGAAGC CATCAAATCA TGCTACCATC	180
CAGAGTATAG TGAGAGCTGT GGGGGTCGTT CCTGGGATTC CTGAGCCTTG CTGTGTACCA	240
GAAAAGATGT CCTCACTCAG TATTTTATTC TTTGATGAAA ATAAGAATGT AGTGCTTAAA	300
GTATACCCTA ACATGACAGT AGAGTCTTGC GCTTGCAGAT AACCTGGCAA AGAACTCATT	360
TGAATGCTTA ATTCAAT	377